

Sequence 7, Appli  
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Sequence 9, Appli  
Sequence 10, Appli

238 3 US-09-005-299-7  
238 3 US-09-515-431-7  
263 2 US-08-768-964-2  
263 3 US-09-005-299-2  
263 3 US-09-515-431-2  
229 3 US-08-833-488B-24  
253 3 US-08-833-488B-20  
227 1 US-07-869-933-14  
227 3 US-09-103-663-14  
222 1 US-07-869-933-12  
222 3 US-09-103-663-12  
222 3 US-09-103-663-28  
222 3 US-09-103-663-12  
201 3 US-09-015-734-12  
201 4 US-09-515-311-12  
199 3 US-08-833-488B-14  
431 4 US-09-592-998C-9  
435 4 US-09-592-998C-10

ALIGNMENTS

RESULT 1  
US-07-869-933-13  
; Sequence 13, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07869,933  
; FILING DATE: 19920416  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: homo sapien  
; STRAIN: FcRI alpha subunit  
; US-07-869-933-13  
Query Match 100.0%; Score 1264; DB 1; Length 232;  
Best Local Similarity 100.0%; Pred. No. 6.5e-115;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VPOKPKVSLNPPWNRIFKGENVTLCNNGNFFVSTKMFHNGSLSEETNSSLNIYNAKF 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.  
OM protein - protein search, using sw model  
Run on: October 6, 2004, 08:59:40 ; Search time 15.1422 Seconds  
(without alignments)  
790.984 Million cell updates/sec

Title: US-10-763-400-6  
Perfect score: 1264  
Sequence: 1 VPOKPKVSLNPPWNRIFKGE.....RTRKGFRLLNPHKPKNPKN 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pap.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1264	100.0	232	1	US-07-869-933-13
2	1264	100.0	232	2	US-08-756-387B-6
3	1264	100.0	232	3	US-09-103-663-13
4	1264	100.0	232	4	US-09-285-873-6
5	1264	100.0	232	4	US-09-944-277A-6
6	1264	100.0	257	1	US-07-869-933-11
7	1264	100.0	257	2	US-08-756-387B-2
8	1264	100.0	257	3	US-09-103-663-11
9	1264	100.0	257	4	US-08-897-956A-1
10	1264	100.0	257	4	US-09-944-277A-2
11	1264	100.0	257	4	US-08-897-956A-3
12	991	78.4	978	4	US-08-756-387B-13
13	947	74.9	172	2	US-09-285-873-13
14	947	74.9	172	4	US-09-245-764-9
15	947	74.9	172	4	US-09-944-277A-13
16	947	74.9	172	4	US-08-756-387B-11
17	947	74.9	197	2	US-09-015-734-7
18	947	74.9	197	4	US-09-285-873-11
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Query Match 100.0%; Score 1264; DB 1; Length 232;  
Best Local Similarity 100.0%; Pred. No. 6.5e-115;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EDSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 2
US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945234
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-6

Query Match 100.0%; Score 1264; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
Db 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
QY 61 EDSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
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Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 3
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinnet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-13

Query Match 100.0%; Score 1264; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.5e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VPQKPKVSLNPPNRIKGENVTLTCNGNFFVSTKWFHNGSLSEETNSLINVNAKF 60
QY 61 EDSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
Db 61 EDSEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
QY 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
Db 121 YKDGALKYWEHNHISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180
QY 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232
Db 181 FFIPLLVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLNPHPKPNPKNN 232

RESULT 4
US-09-285-873-6
; Sequence 6, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
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SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/285,873  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387  
FILING DATE: NO. 6309832ember 26, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-285-873-6

Query Match 100.0%; Score 1264; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 6.5e-115;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSLNVNAKF 60  
DB 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSLNVNAKF 60  
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQSAEVVMEGQPLFLRCHGRNWDVYKVIY 120  
DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQSAEVVMEGQPLFLRCHGRNWDVYKVIY 120  
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180  
DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180  
QY 181 FPIPLVLLFAVDTGFLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232  
DB 181 FPIPLVLLFAVDTGFLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232

RESULT 5  
US-09-944-277A-6  
Sequence 6, Application US/09944277A  
Patent No. 6682894  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
Porter, James P.  
Rushlow, Keith E.  
Wasson, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-944-277A-6

Query Match 100.0%; Score 1264; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 6.5e-115;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSLNVNAKF 60  
DB 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSLNVNAKF 60  
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DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQSAEVVMEGQPLFLRCHGRNWDVYKVIY 120  
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180  
DB 121 YKDGALKYWNHNISITNATVEDSGTYCTGKRWQLDYSEPLNTVIKAPREKYWLQ 180  
QY 181 FPIPLVLLFAVDTGFLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232  
DB 181 FPIPLVLLFAVDTGFLFISTQQQVTFLLKTKRTRKGFRLNPHKPNKNN 232

RESULT 6  
US-07-869-933-11  
Sequence 11, Application US/07869933  
Patent No. 5770396  
GENERAL INFORMATION:  
APPLICANT: KINET, Jean-Pierre  
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
IMMUNOGLOBULIN  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/869,933  
FILING DATE: 19920416  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149

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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-869-933-11

Query Match          100.0%; Score 1264; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 85
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
DB 206 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 257

RESULT 7
US-08-756-387B-2
; Sequence 2, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-2

Query Match          100.0%; Score 1264; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 85
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
DB 206 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 257

RESULT 8
US-09-103-663-11
; Sequence 11, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; EARLIER FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 257
; TYPE: PRI
; ORGANISM: Homo sapiens
; US-09-103-663-11

Query Match          100.0%; Score 1264; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQPKVSLNPPWNRIFKGENVTLCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 85
QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGALKYWNHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
DB 206 FFIPLLVILFAVDTGFLISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 257

RESULT 9
US-09-285-873-2
; Sequence 2, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige

```



```

; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 630932ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-2

Query Match 100.0%; Score 1264; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTITCNGNPFVSSSTKWFHNGSLSEETSSSLNIVNAKF 60
DB 26 VPQPKVSLNPPNRIKGENVTITCNGNPFVSSSTKWFHNGSLSEETSSSLNIVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGKALKYWNENHISITNATVDSGTYYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGKALKYWNENHISITNATVDSGTYYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFLLNPHKPNPKNN 232
DB 206 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFLLNPHKPNPKNN 257

RESULT 11
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-944-277A-2

; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESS: Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 630932ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-285-873-2

Query Match 100.0%; Score 1264; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.4e-115;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTITCNGNPFVSSSTKWFHNGSLSEETSSSLNIVNAKF 60
DB 26 VPQPKVSLNPPNRIKGENVTITCNGNPFVSSSTKWFHNGSLSEETSSSLNIVNAKF 85
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDSGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGKALKYWNENHISITNATVDSGTYYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 180
DB 146 YKDGKALKYWNENHISITNATVDSGTYYCTGKQWQLDYSEPLNITVIKAPREKYWLQ 205
QY 181 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFLLNPHKPNPKNN 232
DB 206 FFIPLLVILFAVDTGFLISTQQQVTFLLKIKRTRKGFLLNPHKPNPKNN 257

RESULT 10
US-08-897-956A-1
; Sequence 1, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
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Query Match 100.0%; Score 1264; DB 4; Length 257;  
Best Local Similarity 100.0%; Pred. No. 7.4e-115; Indels 0; Gaps 0;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGNVTLTCGNNPFVSTKWFHNGSLSEETNSLNIIVNAKF 60  
DB 26 VPQKPKVSLNPPWNRIFKGNVTLTCGNNPFVSTKWFHNGSLSEETNSLNIIVNAKF 85  
QY 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
DB 86 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145  
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYESEPLNITVIKAPREKYWLQ 180  
DB 146 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYESEPLNITVIKAPREKYWLQ 205  
QY 181 FTPLLVILFAVDTGLFISTQOQVTFLLKIKRTRKGRFLLNPHPKPNKPN 232  
DB 206 FTPLLVILFAVDTGLFISTQOQVTFLLKIKRTRKGRFLLNPHPKPNKPN 257

## RESULT 12

US-08-897-956A-3  
; Sequence 3, Application US/08897956A  
; Patent No. 6423512  
; GENERAL INFORMATION:  
; APPLICANT: Mary Ellen Digan  
; APPLICANT: Philip Lake  
; APPLICANT: Hermann Gram  
; TITLE OF INVENTION: Fusion Polypeptides  
; FILE REFERENCE: 600-7244/CPA  
; CURRENT APPLICATION NUMBER: US/08/897,956A  
; CURRENT FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: 60/022,689  
; PRIOR FILING DATE: 1996-07-26  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 978  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion polypeptide  
US-08-897-956A-3

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Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 26 VPQKPKVSLNPPWNRIFKGNVTLTCGNNPFVSTKWFHNGSLSEETNSLNIIVNAKF 85  
QY 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
DB 86 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145  
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYESEPLNITVIKAPREKYWL 179  
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## RESULT 13

US-08-756-387B-13  
; Sequence 13, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 172 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-756-387B-13

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QY 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
DB 61 EDGSEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKVMQDYESEPLNITVIK 172  
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## RESULT 14

US-09-285-873-13  
; Sequence 13, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA: ..  
APPLICATION NUMBER: US/09/285,873  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387  
FILING DATE: No. 6309332ember 26, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: verser, Carol talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 172 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-285-873-13

Query Match 74.9%; Score 947; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 2.5e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 EDSGEYKCOHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
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RESULT 15  
US-09-245-764-9  
Sequence 9, Application US/09245764  
Patent No. 6675105  
GENERAL INFORMATION:  
APPLICANT: Hogarth, P. Mark  
APPLICANT: Powell, Maree S.  
APPLICANT: McKenzie, Ian F.C.  
APPLICANT: Maxwell, Kelly F.  
APPLICANT: Garrett, Thomas P.J.  
APPLICANT: Epa, Vicana  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS  
FILE REFERENCE: 4102-4  
CURRENT APPLICATION NUMBER: US/09/245,764  
CURRENT FILING DATE: 1999-02-05  
EARLIER APPLICATION NUMBER: 60/099,994  
EARLIER FILING DATE: 1998-09-11  
EARLIER APPLICATION NUMBER: 60/073,972  
EARLIER FILING DATE: 1998-02-06  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 9  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-245-764-9

Query Match 74.9%; Score 947; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 2.5e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 70.8438 Seconds  
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Gapop 10.0 , Gapext 0.5

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Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1264	100.0	257	12 US-10-236-392-28	Sequence 28, Appli
4	1264	100.0	257	14 US-10-384-850-45	Sequence 45, Appli
5	1031.5	81.6	218	12 US-10-236-392-30	Sequence 30, Appli
6	969	76.7	176	10 US-09-809-715-2	Sequence 2, Appli
7	969	76.7	176	12 US-10-293-992-2	Sequence 2, Appli
8	947	74.9	172	9 US-09-944-277A-13	Sequence 13, Appli
9	947	74.9	172	9 US-09-245-764-9	Sequence 9, Appli
10	947	74.9	172	12 US-10-293-992-4	Sequence 4, Appli
11	947	74.9	172	12 US-10-687-109-9	Sequence 9, Appli
12	947	74.9	197	9 US-09-944-277A-11	Sequence 11, Appli
13	944	74.7	176	10 US-09-809-715-4	Sequence 4, Appli
14	785.5	62.1	236	15 US-10-434-817-7	Sequence 7, Appli
15	785.5	62.1	255	15 US-10-434-817-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-944-277A-6  
Sequence 6, Application US/09944277A  
Patent No. US20020034771A1  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
Porter, James P.  
Rushlow, Keith E.  
Wasom, Donald E.  
TITLE OF INVENTION: Method to Detect IGE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Carol Talkington Verser, Ph.D.  
Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505

Sequence 12, Appli  
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US-10-183-377-6  
US-10-027-736A-9  
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US-10-027-736A-10  
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US-10-183-377-7  
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US-10-027-736A-18  
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

Query Match          100.0%; Score 1264; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.3e-101; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

QY 1 VPQPKVSLNPPWNRIFKGNVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 60
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Db 1 VPQPKVSLNPPWNRIFKGNVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 60
   |||||

QY 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
   |||||
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
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   |||||
Db 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 180
   |||||

QY 181 FFIPLLVILFAVDLTGLFISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
   |||||
Db 181 FFIPLLVILFAVDLTGLFISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
   |||||

RESULT 2
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match          100.0%; Score 1264; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.7e-101; Indels 0; Gaps 0;
Matches 232; Conservative 0; Mismatches 0;

QY 1 VPQPKVSLNPPWNRIFKGNVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 60
   |||||
Db 26 VPQPKVSLNPPWNRIFKGNVTLTCGNNFFEVSTKWFHNGSLSEETNSLNIYNAKF 85
   |||||

QY 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 120
   |||||
Db 86 EDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNDVYKVIY 145
   |||||

QY 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 180
   |||||
Db 146 YKDGEALKWYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 205
   |||||

QY 181 FFIPLLVILFAVDLTGLFISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 232
   |||||
Db 206 FFIPLLVILFAVDLTGLFISTQQVTFLLKIKRTRKGFLLNPHPKPNPKNN 257
   |||||

RESULT 3
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glenda
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
```

PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: US60/367,753  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: US60/369,479  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US09/659,634  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: US60/318,120  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: US60/318,130  
PRIOR FILING DATE: 2001-09-07  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 794  
SOFTWARE: Custom  
SEQ ID NO 28  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-236-392-28

Query Match 100.0%; Score 1264; DB 12; Length 257;  
Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQSAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
Db 86 EDSEYKCOHQVNESEPVYLEVFSDDLLOQSAEVVMGQPLFLRCHGWRNWDVYKVIY 145

Qy 121 YKGEALKYVYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180  
Db 146 YKGEALKYVYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVVLPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHKPNKNN 232  
Db 206 FFIPLLVVLPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHKPNKNN 257

## RESULT 4

US-10-384-850-45  
Sequence 45, Application US/10384850  
Publication No. US20030175890A1  
GENERAL INFORMATION:  
APPLICANT: C. Fraser  
TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF  
CURRENT FILING DATE: 2003-03-21  
PRIOR APPLICATION NUMBER: US/10/384,850  
CURRENT FILING DATE: 2003-03-10  
PRIOR APPLICATION NUMBER: US/09/702,021  
PRIOR FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 45  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-384-850-45

Query Match 100.0%; Score 1264; DB 14; Length 257;  
Best Local Similarity 100.0%; Pred. No. 3.7e-101;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy 61 EDSEYKCOHQVNESEPVYLEVFSDDLLOQSAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
Db 86 EDSEYKCOHQVNESEPVYLEVFSDDLLOQSAEVVMGQPLFLRCHGWRNWDVYKVIY 145

Qy 121 YKGEALKYVYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 180  
Db 146 YKGEALKYVYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVVLPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHKPNKNN 232  
Db 206 FFIPLLVVLPAVDTGFIQTQQVTFLLKIKRTRKGRFLLNPHKPNKNN 257

RESULT 5  
US-10-236-392-30  
Sequence 30, Application US/10236392  
Publication No. US20040067490A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Burgess, Catherine, E  
APPLICANT: Casman, Stacie J  
APPLICANT: Catterton, Elina  
APPLICANT: Chapoval, Andrei  
APPLICANT: Crabtree, Julie  
APPLICANT: Edinger, Shlomit, R  
APPLICANT: Ellerman, Karen  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Grosse, William M  
APPLICANT: Gusev, Vladimir  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Laroche, William J  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Miller, Charles E  
APPLICANT: Millet, Isabelle  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol A  
APPLICANT: Peyman, John A  
APPLICANT: Rastelli, Luca  
APPLICANT: Reiger, Daniel K  
APPLICANT: Rothenberg, Mark E  
APPLICANT: Shenoy, Suresh  
APPLICANT: Shinkets, Richard A  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-442A  
CURRENT APPLICATION NUMBER: US/10/236,392  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US09/540,763  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: US60/390,155  
PRIOR FILING DATE: 2002-06-19  
PRIOR APPLICATION NUMBER: US09/635,949  
PRIOR FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: US60/318,765  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US60/357,303  
PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: US60/367,753  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: US60/369,479  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US09/659,634  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: US60/318,120  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: US60/318,130  
PRIOR FILING DATE: 2001-09-07  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 794  
SOFTWARE: Custom  
SEQ ID NO 30  
LENGTH: 218

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-236-392-30

Query Match 81.6%; Score 1031.5; DB 12; Length 218;  
Best Local Similarity 83.2%; Pred. No. 3.8e-81;  
Matches 193; Conservative 0; Mismatches 0; Indels 39; Gaps 1;  
  
QY 1 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 60  
DB 26 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 85  
QY 61 EDSGEYKCOHQVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
DB 86 EDSGEYK-----CHGWRNDVYKVIY 106  
QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYLQ 180  
DB 107 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREKYLQ 166  
QY 181 FPIPLLVILFAVDGLFTSTQQQVTFLLKIKRTKGRFLLNPHPKPNKN 232  
DB 167 FPIPLLVILFAVDGLFTSTQQQVTFLLKIKRTKGRFLLNPHPKPNKN 218

## RESULT 6

US-09-809-715-2  
; Sequence 2, Application US/09809715  
; Publication No. US20030003502A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Wurzburg, Beth A.  
; APPLICANT: Kinet, Jean-Pierre  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC  
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE  
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF  
; FILE REFERENCE: AL-8  
; CURRENT APPLICATION NUMBER: US/09/809,715  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,853  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-715-2

Query Match 76.7%; Score 969; DB 10; Length 176;  
Best Local Similarity 100.0%; Pred. No. 7.5e-76;  
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 60  
DB 1 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 60  
QY 61 EDSGEYKCOHQVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
DB 61 EDSGEYKCOHQVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176  
DB 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176

## RESULT 7

US-10-293-992-2  
; Sequence 2, Application US/10293992  
; Publication No. US200400033527A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.

; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Kinet, Jean-Pierre  
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR  
; TITLE OF INVENTION: CHAIN  
; FILE REFERENCE: AL-3-C1-1  
; CURRENT APPLICATION NUMBER: US/10/293,992  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/434,193  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,219  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-992-2

Query Match 76.7%; Score 969; DB 12; Length 176;

Best Local Similarity 100.0%; Pred. No. 7.5e-76;  
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 60  
DB 1 VPQPKVSLNPPNRIKGENVTLTCGNNPFEVSTKWFHNGSLSEETNSLNINAKF 60  
QY 61 EDSGEYKCOHQVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
DB 61 EDSGEYKCOHQVNESEPVYLEVSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
QY 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176  
DB 121 YKDGALKYWHNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKAPREK 176

## RESULT 8

US-09-944-277A-13  
; Sequence 13, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272



TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 172 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-944-277A-13

Query Match 74.9%; Score 947; DB 9; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 DB 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 QY 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 9  
 US-09-245-764-9  
 ; Sequence 9, Application US/09245764  
 ; Patent No. US20020107359A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hogarth, P. Mark  
 ; APPLICANT: Powell, Maree S.  
 ; APPLICANT: McKenzie, Ian F.C.  
 ; APPLICANT: Maxwell, Kelly F.  
 ; APPLICANT: Garrett, Thomas P.J.  
 ; APPLICANT: Epa, Vidana  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS  
 ; FILE REFERENCE: 4102-4  
 ; CURRENT APPLICATION NUMBER: US/09/245,764  
 ; EARLIER FILING DATE: 1999-02-05  
 ; EARLIER FILING DATE: 1998-09-11  
 ; EARLIER APPLICATION NUMBER: 60/099,994  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 172  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-245-764-9

Query Match 74.9%; Score 947; DB 9; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 DB 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 QY 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 10

US-10-293-992-4  
 ; Sequence 4, Application US/10293992  
 ; Publication No. US20040033527A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jaretzky, Theodore S.  
 ; APPLICANT: Garman, Scott Clayton  
 ; APPLICANT: Kinet, Jean-Pierre  
 ; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPTOR  
 ; FILE REFERENCE: AL-3-C1-1  
 ; CURRENT APPLICATION NUMBER: US/10/293,992  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: 09/434,193  
 ; PRIOR FILING DATE: 1999-11-04  
 ; PRIOR APPLICATION NUMBER: 60/107,219  
 ; PRIOR FILING DATE: 1998-11-05  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 172  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-293-992-4

Query Match 74.9%; Score 947; DB 12; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 DB 1 VPQKPKVSLNPPWRIKGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKF 60  
 QY 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDSEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 11  
 US-10-687-109-9  
 ; Sequence 9, Application US/10687109  
 ; Publication No. US20040054480A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hogarth, P. Mark  
 ; APPLICANT: Powell, Maree S.  
 ; APPLICANT: McKenzie, Ian F.C.  
 ; APPLICANT: Maxwell, Kelly F.  
 ; APPLICANT: Garrett, Thomas P.J.  
 ; APPLICANT: Epa, Vidana  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS  
 ; FILE REFERENCE: 4102-4  
 ; CURRENT APPLICATION NUMBER: US/10/687,109  
 ; CURRENT FILING DATE: 2003-10-15  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 172  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-687-109-9

Query Match 74.9%; Score 947; DB 12; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-74;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 120  
Db 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 120  
QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172  
Db 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

## RESULT 12

US-09-944-277A-11

; Sequence 11, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944.277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 197 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-944-277A-11

## Query Match

Best Local Similarity 100.0%; Pred. No. 6.9e-74;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 26 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 85  
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 120  
Db 86 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 145

QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172  
Db 146 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197

## RESULT 13

US-09-809-715-4

; Sequence 4, Application US/09809715

; Publication No. US2003000302A1

; GENERAL INFORMATION:

; APPLICANT: Jaretzky, Theodore S.

; Garman, Scott Clayton

; APPLICANT: Wurzburg, Beth A.

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC

; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN Ige

; FILE REFERENCE: AL-8

; CURRENT APPLICATION NUMBER: US/09/809,715

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: 60/189,853

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 176

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-809-715-4

Query Match 74.7%; Score 944; DB 10; Length 176;

Best Local Similarity 97.7%; Pred. No. 1.1e-73;

Matches 172; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 1 VPQKPKVSLNPPNRRIFKGNVTLTCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
QY 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 120  
Db 61 EDSGEYKCHQOQVNESEPVYLEVFSDDLLOQSAEAVVMEGQPLFLRCHGWRNDVYKVIY 120  
QY 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKAPREK 176  
Db 121 YKDGKALKYWNHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKAPREK 176

## RESULT 14

US-10-434-817-7

; Sequence 7, Application US/10434817

; Publication No. US20030235579A1

; GENERAL INFORMATION:

; APPLICANT: Weber, Eric R.

; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA

; CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heska Corporation

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/434,817

; FILING DATE: 08-May-2003

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,734  
FILING DATE: 29-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-434-817-2  
Query Match 62.1%; Score 785.5; DB 15; Length 236;  
Best Local Similarity 66.2%; Pred. No. 7.9e-60;  
Matches 151; Conservative 29; Mismatches 43; Indels 5; Gaps 2;  
QY 3 QKPKVSLNPPWNRIFKGENVLTCTGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKPED 62  
DB 9 RKSTVSLNPPWNRIFKGENVLTCTGNNKPLKGNSTEWYNTTLEVTSSLNITNASHRS 68  
QY 63 SGKYKCHOQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGMRNDVYKVIYK 122  
DB 69 SGYRCRNDNLSEAVHLEVFSDWLLLOASAEVIEGKALVLCRCGWKDWDFKVIYK 128  
QY 123 DGEALKYWNHNISITNATVEDSGTYCTG-----KWQLDYSEPLNITVIKAPREK-Y 177  
DB 129 DGKPLEYWNKNISIESATENSSTYCEGAFNFKRTSERYTSDYLNITVKKAEQSKRY 188  
QY 178 WLOFFIPLLVILLFAVDTLGTFISTQQQVTFLLKIKRTRKGFRLNPHP 225  
DB 189 WLOFIPLLVILLFAVDTLGTFVSTQQQLTFLLKIKRTRGRKLMDEHP 236  
RESULT 15  
US-10-434-817-2  
Sequence 2, Application US/10434817  
Publication No. US20030235579A1  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
McCall, Catherine A.  
TITLE OF INVENTION: NOVEL EQUINE FC EPSILON RECEPTOR ALPHA  
CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/434,817  
FILING DATE: 08-May-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,734  
FILING DATE: 29-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-434-817-2  
Query Match 62.1%; Score 785.5; DB 15; Length 255;  
Best Local Similarity 66.2%; Pred. No. 8.6e-60;  
Matches 151; Conservative 29; Mismatches 43; Indels 5; Gaps 2;  
QY 3 QKPKVSLNPPWNRIFKGENVLTCTGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKPED 62  
DB 28 RKSTVSLNPPWNRIFKGENVLTCTGNNKPLKGNSTEWYNTTLEVTSSLNITNASHRS 87  
QY 63 SGKYKCHOQVNESEPVYLEVFSDWLLLOASAEVVMGQPLFLRCHGMRNDVYKVIYK 122  
DB 88 SGYRCRNDNLSEAVHLEVFSDWLLLOASAEVIEGKALVLCRCGWKDWDFKVIYK 147  
QY 123 DGEALKYWNHNISITNATVEDSGTYCTG-----KWQLDYSEPLNITVIKAPREK-Y 177  
DB 148 DGKPLEYWNKNISIESATENSSTYCEGAFNFKRTSERYTSDYLNITVKKAEQSKRY 207  
QY 178 WLOFFIPLLVILLFAVDTLGTFISTQQQVTFLLKIKRTRKGFRLNPHP 225  
DB 208 WLOFIPLLVILLFAVDTLGTFVSTQQQLTFLLKIKRTRGRKLMDEHP 255

Search completed: October 6, 2004, 09:28:10  
Job time : 71.8438 secs

*This Page Blank (uspto)*

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 12.7086 Seconds  
(without alignments)  
1756.007 Million cell updates/sec

Title: US-10-763-400-6  
Perfect score: 1264  
Sequence: 1 VPQPKVSLNPPNRIKFGZ.....RTRKGFLLNPPKPNPKNN 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

- 1: pir1.\*
- 2: pir2.\*
- 3: pir3.\*
- 4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1364	100.0	257	2 S00682	IgE Fc receptor precursor - human
2	587.5	46.5	250	2 A34342	IgE Fc receptor precursor - human
3	576.5	45.6	245	2 A30154	IgE Fc receptor precursor - human
4	411.5	32.6	254	1 J10107	FC gamma (Igg) rec
5	399.5	31.6	233	1 J10284	FC gamma (Igg) rec
6	398.5	31.5	280	2 I55577	FC gamma (Igg) rec
7	390	30.9	267	2 A35902	FC gamma (Igg) rec
8	389	30.8	267	2 I56110	FC gamma (Igg) rec
9	387.5	30.7	261	2 S29360	FC gamma (Igg) rec
10	381	30.1	296	2 I46021	FC gamma (Igg) rec
11	375	29.7	267	2 I72882	FC gamma (Igg) rec
12	371.5	29.4	344	2 A41357	FC gamma (Igg) rec
13	371.5	29.4	374	1 A39878	FC gamma (Igg) rec
14	369	29.2	336	2 I48471	FC gamma (Igg) rec
15	369	29.2	404	2 A46480	FC gamma (Igg) rec
16	367	29.0	270	2 A34636	FC gamma (Igg) rec
17	363.5	28.8	283	1 FCMSQ1	FC gamma (Igg) rec
18	363.5	28.8	330	2 A40071	FC gamma (Igg) rec
19	363.5	28.8	330	2 I49660	FC gamma (Igg) rec
20	361.5	28.6	285	2 S36903	FC gamma (Igg) rec
21	345	27.3	323	2 S06946	FC gamma (Igg) rec
22	341	27.0	310	2 J10119	FC gamma (Igg) rec
23	338	26.7	160	2 I47163	cytolytic trigger
24	328	25.9	317	2 J10118	FC gamma (Igg) rec
25	327	25.9	157	2 D31327	IgE receptor alpha
26	271	21.4	159	2 I47164	cytolytic trigger
27	162.5	12.9	1694	2 S50065	sialoadhesin - mou
28	148	11.7	104	2 I47165	cytolytic trigger
29	137.5	10.9	458	1 WWSR1	biliary glycoprote

30	137.5	10.9	521	2 JC1508	biliary glycoprote
31	136.5	10.8	458	2 JC1509	biliary glycoprote
32	136.5	10.8	458	2 S21969	cell-adhesion mole
33	136.5	10.8	458	2 S68177	C-CAM2a protein is
34	136.5	10.8	519	2 A44783	ecto-ArPase precu
35	136.5	10.8	521	2 S4338	biliary glycoprote
36	134	10.6	7962	2 JC2457	elastic titin - hu
37	131	10.4	538	2 JC2457	vascular cell adhe
38	129.5	10.2	344	2 A27681	neuroglial - fruit
39	129.5	10.2	1239	1 A32579	cell adhesion prot
40	123	9.7	1033	2 S19247	immunoglobulin-li
41	122	9.7	1327	2 T09402	CD22 homolog/B lym
42	121	9.6	868	2 A46512	vascular cell adhe
43	120.5	9.5	739	2 JS0675	B-cell adhesion pr
44	120	9.5	647	2 A35648	differentiation an
45	120	9.5	862	2 I49583	

#### ALIGNMENTS

##### RESULT 1

S00682  
IGF Fc receptor alpha chain precursor - human  
N:Alternate names: Fc-epsilon receptor  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text\_change 23-Jul-1999  
C:Accession: S00682; B30154; S42209  
R:Kochan, J.; Pettine, L.F.; Hakim, J.; Kishi, K.; Kinet, J.P.  
Nucleic Acids Res. 16, 3584, 1988  
A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity  
A:Reference number: S00682; MUID:88233953; PMID:2967464  
A:Accession: S00682  
A:Molecule type: mRNA  
A:Residues: 1-257 <KOC>  
A:Cross-references: EMBL:X05948; NID:g31317; PIDN:CAA30025.1; PID:g31318  
R:Shimizu, A.; Tepfer, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characteriza  
A:Reference number: A34191; MUID:88158102; PMID:2964640  
A:Accession: B30154  
A:Molecule type: mRNA  
A:Residues: 1-257 <SH>  
A:Cross-references: GB:J03605; NID:gi87449; PIDN:AAA36204.1; PID:g307164  
R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.  
Eur. J. Biochem. 220, 593-598, 1994  
A:Title: High-level expression of the truncated alpha chain of human high-affinity recei  
nant product.  
A:Reference number: S42209; MUID:94170811; PMID:8125119  
A:Accession: S42209  
A:Molecule type: protein  
A:Residues: 26-197 <YAG>  
A:Experimental source: purified recombinant protein  
C:Genetics:  
A:Gene: GDB:FCER1A  
A:Cross-references: GDB:I119902; OMIM:147140  
A:Map Position: 1q23-1q23  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: immunoglobulin receptor; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <sig>  
F:26-257/Product: IGF Fc receptor alpha chain #status predicted <KAT>  
F:44-95/Domain: immunoglobulin homology <IMM1>  
F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 1264; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 2.1e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRIKFGZVTITCNNGNFFVSSTKPFHNGSLSEETNSSLNINAKF 60  
Db 26 VPQPKVSLNPPNRIKFGZVTITCNNGNFFVSSTKPFHNGSLSEETNSSLNINAKF 85  
QY 61 EDSSEYKQCHQVNESEPVYLEVFSDWLLQLQAEVVMCEQPLFLRCHGRWHDVTKVIY 120

Db 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWEGQPLFURCHGRNWDVYKVIY 145  
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKAPREKYWLQ 180  
 Db 146 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKAPREKYWLQ 205  
 QY 181 FFIPLVVLPAVDVGLFISTQCOQVTFLLKIKRFGRLNPHKPNKPN 232  
 Db 206 FFIPLVVLPAVDVGLFISTQCOQVTFLLKIKRFGRLNPHKPNKPN 257

## RESULT 2

A:Residues: 1-245 <LIU>  
 A:Cross-references: GB:M21622; GB:J03811  
 A:Experimental source: basophilic leukemia cell line, clone R3-4  
 A:Accession: A31327  
 A:Molecule type: mRNA  
 A:Residues: 21-245 <L13>  
 A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811  
 A:Experimental source: basophilic leukemia cell line  
 R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
 A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization  
 A:Reference number: A94191; MUID:88158102; PMID:2964640  
 A:Accession: A30154  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <SHI>  
 A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332  
 R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.  
 Biochemistry 26, 4605-4610, 1987  
 A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff  
 A:Reference number: A27116; MUID:88024987; PMID:2959318  
 A:Accession: A27116  
 A:Molecule type: mRNA  
 A:Residues: 1, 'G', '3-236, 'N', '238-244, 'RLKPNS' <KIN>  
 R:Tepler, I.; Shimizu, A.; Leder, P.  
 J. Biol. Chem. 264, 5912-5915, 1989  
 A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur  
 A:Reference number: I55304; MUID:89174653; PMID:2522441  
 A:Accession: I53304  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>  
 F:42-93/Domain: immunoglobulin homology <IMM>

Query Match 46.5%; Score 587.5; DB 2; Length 250;  
 Best Local Similarity 52.3%; Pred. No. 4e-39;  
 Matches 113; Conservative 43; Mismatches 57; Indels 3; Gaps 3;

QY 3 QKPKVSLNPPNRIKGENVTLCNGNPFVEV-SSTKWFNGSLSEETNSLNIIVNAKFE 61  
 Db 26 EKSVLTLDPPIRFTGKVTLSYGNHLMQNSTTKWIHNGTVSEVNSHLVIVSATVQ 85  
 QY 62 DSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWEGQPLFURCHGRNWDVYKVIY 121  
 Db 86 DSGYIKCQKGLFKSPVLYNTQDWLLQTSADMLVHGSFDIRCHGRNWRKVIY 145  
 QY 122 KDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKAPREK-YWLQ 180  
 Db 146 RNDHAFNYSES-PVSIREATLNDSTGYHCKGYLRQVEYSDKFRFIAVAVKAYCKYWLQ 204  
 QY 181 FFIPLVVLPAVDVGLFISTQCOQVTFLLKIKRTRK 216  
 Db 205 LIFPLVAILPAVDVGLLSTEEQFKSVLEIQTKG 240

## RESULT 3

A:Residues: 1-245 <LIU>  
 A:Cross-references: GB:M21622; GB:J03811  
 A:Experimental source: basophilic leukemia cell line, clone R3-4  
 A:Accession: A31327  
 A:Molecule type: mRNA  
 A:Residues: 21-245 <L13>  
 A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811  
 A:Experimental source: basophilic leukemia cell line  
 R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
 A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization  
 A:Reference number: A94191; MUID:88158102; PMID:2964640  
 A:Accession: A30154  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <SHI>  
 A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332  
 R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.  
 Biochemistry 26, 4605-4610, 1987  
 A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff  
 A:Reference number: A27116; MUID:88024987; PMID:2959318  
 A:Accession: A27116  
 A:Molecule type: mRNA  
 A:Residues: 1, 'G', '3-236, 'N', '238-244, 'RLKPNS' <KIN>  
 R:Tepler, I.; Shimizu, A.; Leder, P.  
 J. Biol. Chem. 264, 5912-5915, 1989  
 A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur  
 A:Reference number: I55304; MUID:89174653; PMID:2522441  
 A:Accession: I53304  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>  
 F:42-93/Domain: immunoglobulin homology <IMM>

A:Residues: 1-245 <LIU>  
 A:Cross-references: GB:M21622; GB:J03811  
 A:Experimental source: basophilic leukemia cell line, clone R3-4  
 A:Accession: A31327  
 A:Molecule type: mRNA  
 A:Residues: 21-245 <L13>  
 A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811  
 A:Experimental source: basophilic leukemia cell line  
 R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
 A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization  
 A:Reference number: A94191; MUID:88158102; PMID:2964640  
 A:Accession: A30154  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <SHI>  
 A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332  
 R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.  
 Biochemistry 26, 4605-4610, 1987  
 A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff  
 A:Reference number: A27116; MUID:88024987; PMID:2959318  
 A:Accession: A27116  
 A:Molecule type: mRNA  
 A:Residues: 1, 'G', '3-236, 'N', '238-244, 'RLKPNS' <KIN>  
 R:Tepler, I.; Shimizu, A.; Leder, P.  
 J. Biol. Chem. 264, 5912-5915, 1989  
 A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur  
 A:Reference number: I55304; MUID:89174653; PMID:2522441  
 A:Accession: I53304  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>  
 F:42-93/Domain: immunoglobulin homology <IMM>

Query Match 45.6%; Score 576.5; DB 2; Length 245;  
 Best Local Similarity 51.4%; Pred. No. 2.9e-38;  
 Matches 111; Conservative 39; Mismatches 65; Indels 1; Gaps 1;

QY 3 QKPKVSLNPPNRIKGENVTLCNGNPFVEV-SSTKWFNGSLSEETNSLNIIVNAKFE 62  
 Db 26 QKSVVSLDPPPIRILTGDKVTLCNGNNSQNSTKWIHNDISINVKSSHVIVSATIQD 85  
 QY 63 DSGEYKCOHQVNESEPVYLEVFSDDLQASAEVWEGQPLFURCHGRNWDVYKVIY 122  
 Db 86 DSGYIKCQKGLFKSPVLYNTQDWLLQTSADMLVHGSFDIRCHGRNWRKVIY 145  
 QY 123 DGEALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKAPREK-YWLQ 181  
 Db 146 DDIAFKSYSDSNISIRKATFNDSTGYHCKGYLRQVEYSDKFRFIAVAVKAYCKYWLQ 205  
 QY 182 FFIPLVVLPAVDVGLFISTQCOQVTFLLKIKRTRK 217  
 Db 206 IFPSLAVILPAVDVGLFSTHQPESILKIQTKG 241

## RESULT 4

A:Residues: 1-245 <LIU>  
 A:Cross-references: GB:M21622; GB:J03811  
 A:Experimental source: basophilic leukemia cell line, clone R3-4  
 A:Accession: A31327  
 A:Molecule type: mRNA  
 A:Residues: 21-245 <L13>  
 A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811  
 A:Experimental source: basophilic leukemia cell line  
 R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
 A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization  
 A:Reference number: A94191; MUID:88158102; PMID:2964640  
 A:Accession: A30154  
 A:Molecule type: mRNA  
 A:Residues: 1-245 <SHI>  
 A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332  
 R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.  
 Biochemistry 26, 4605-4610, 1987  
 A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff  
 A:Reference number: A27116; MUID:88024987; PMID:2959318  
 A:Accession: A27116  
 A:Molecule type: mRNA  
 A:Residues: 1, 'G', '3-236, 'N', '238-244, 'RLKPNS' <KIN>  
 R:Tepler, I.; Shimizu, A.; Leder, P.  
 J. Biol. Chem. 264, 5912-5915, 1989  
 A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur  
 A:Reference number: I55304; MUID:89174653; PMID:2522441  
 A:Accession: I53304  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <RES>  
 A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor; transmembrane protein  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>  
 F:42-93/Domain: immunoglobulin homology <IMM>

C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text\_change 28-Jan-2000  
C;Accession: J00284; S00758; I37628; B32933; A31460  
R;Ravetch, J.V.; Perussia, B.  
J. Exp. Med. 170, 481-497, 1989  
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells  
A;Reference number: J00107; MUID:89328325; PMID:2526846  
A;Accession: J00284  
A;Molecule type: mRNA  
A;Residues: 1-201,'SF',204-233 <RAV>  
A;Cross-references: GB:J04162  
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, di  
rboxyl and  
R;Simmons, D.; Seed, B.  
Nature 333, 568-570, 1988  
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane  
A;Reference number: S00758; MUID:88232937; PMID:2967436  
A;Accession: S00758  
A;Molecule type: mRNA  
A;Residues: 1-233 <SIM>  
A;Cross-references: EMBL:X07934; NID:929744; PIDN:CAA30758.1; PID:G29745  
R;Gessner, J.E.; Grusenmeyer, T.; Kolanus, W.; Schmidt, R.E.  
J. Biol. Chem. 270, 1350-1361, 1995  
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole  
A;Reference number: A55439; MUID:95138131; PMID:7836402  
A;Accession: I37628  
A;Molecule type: DNA  
A;Residues: 1-72 <RES>  
A;Cross-references: EMBL:Z46223; NID:9559446; PIDN:CAA86296.1; PID:9871306  
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989  
C;Comment: This low affinity IgG Fc receptor of natural killer cells, which is the produ  
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in  
C;Genetics:  
A;Gene: GDB:FCGR3A; FCGR3  
A;Cross-references: GDB:I119904; OMIM:146740  
A;Map position: 1q23-1q23  
A;Introns: 14/1; 21/1  
A;Note: the list of introns is incomplete  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: Glycoprotein; receptor; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-254/Product: Fc gamma (IgG) receptor III-A #status experimental <MAT>  
F;18-208/Domain: extracellular #status predicted <EXT>  
F;40-91/Domain: immunoglobulin homology <IMM1>  
F;111-174/Domain: immunoglobulin homology <IMM2>  
F;209-229/Domain: transmembrane #status predicted <TR>  
F;230-254/Domain: intracellular #status predicted <CY>  
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 32.6%; Score 411.5; DB 1; Length 254;  
Best Local Similarity 41.6%; Pred. No. 3e-25;  
Matches 87; Conservative 33; Mismatches 82; Indels 7; Gaps 1;  
QY 4 KPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSSLNIVNAKFEDS 63  
DB 25 KAVVLEPQWYVLEKDSVTLKCGAYSPEDNSTOWFHNESLSSQASSYFIDAATVDDS 84  
QY 64 GEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWNNVDVYKYKD 123  
DB 85 GEYRCQTNLTSLDPVQLEVHIGWLLLOQAPRWFKEDDPHLRCHSKWNTALHKVTYLN 144  
QY 124 GEALKYWEHNIITNATVEDSGTYCTYCTGKWQLDYSEPLNITVTKAPREKYLQFFI 183  
DB 145 GKGRKYHNHSDFYIPRATLKDSGSGYFCRGLFGSKNVSSTVNTITQGLAVSTISSFFP 204  
QY 184 P-----LLVVLPAVDTGFLSTQQOV 205  
DB 205 PGYQVSCFLVMVLLFAVDTGFLFSVKNTNI 233  
RESULT 5  
J00284  
Fc gamma (IgG) receptor III-B precursor (neutrophil) - human  
N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra  
C;Species: Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text\_change 28-Jan-2000  
C;Accession: J00284; S00758; I37628; B32933; A31460  
R;Ravetch, J.V.; Perussia, B.  
J. Exp. Med. 170, 481-497, 1989  
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells  
A;Reference number: J00107; MUID:89328325; PMID:2526846  
A;Accession: J00284  
A;Molecule type: mRNA  
A;Residues: 1-201,'SF',204-233 <RAV>  
A;Cross-references: GB:J04162  
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, di  
rboxyl and  
R;Simmons, D.; Seed, B.  
Nature 333, 568-570, 1988  
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane  
A;Reference number: S00758; MUID:88232937; PMID:2967436  
A;Accession: S00758  
A;Molecule type: mRNA  
A;Residues: 1-233 <SIM>  
A;Cross-references: EMBL:X07934; NID:929744; PIDN:CAA30758.1; PID:G29745  
R;Gessner, J.E.; Grusenmeyer, T.; Kolanus, W.; Schmidt, R.E.  
J. Biol. Chem. 270, 1350-1361, 1995  
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole  
A;Reference number: A55439; MUID:95138131; PMID:7836402  
A;Accession: I37628  
A;Molecule type: DNA  
A;Residues: 1-72 <RES>  
A;Cross-references: EMBL:Z46223; NID:9559446; PIDN:CAA86296.1; PID:9871306  
R;Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989  
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph  
A;Reference number: A32933; MUID:89296947; PMID:2525780  
A;Accession: B32933  
A;Molecule type: mRNA  
A;Residues: 1-121,'E',123-150,'S',152-233 <SCA>  
A;Cross-references: GB:M24854; NID:9184851; PIDN:AAA53507.1; PID:G306930  
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989  
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal  
A;Reference number: A31460; MUID:89128838; PMID:2521732  
A;Accession: A31460  
A;Molecule type: mRNA  
A;Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>  
A;Cross-references: GB:J04162; NID:9183036; PIDN:AAA35881.1; PID:G183037  
C;Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the  
1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod  
C;Genetics:  
A;Gene: GDB:FCGR3B; FCGR3  
A;Cross-references: GDB:I28176; OMIM:146740  
A;Map position: 1q23-1q23  
A;Introns: 14/1; 21/1  
A;Note: the list of introns is incomplete  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linka  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>  
F;40-91/Domain: immunoglobulin homology <IMM1>  
F;111-174/Domain: immunoglobulin homology <IMM2>  
F;56,63,92,92,130,187/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form  
Query Match 31.6%; Score 399.5; DB 1; Length 233;  
Best Local Similarity 41.1%; Pred. No. 2.4e-24;  
Matches 86; Conservative 32; Mismatches 84; Indels 7; Gaps 1;  
QY 4 KPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSSLNIVNAKFEDS 63  
DB 25 KAVVLEPQWYVLEKDSVTLKCGAYSPEDNSTOWFHNESLSSQASSYFIDAATVDDS 84  
QY 64 GEYKCOHQVNESEPVYLEVFSWLLLOQASAEVVMGQPLFLRCHGWNNVDVYKYKD 123  
DB 85 GEYRCQTNLTSLDPVQLEVHIGWLLLOQAPRWFKEDDPHLRCHSKWNTALHKVTYLN 144





C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S29360, S46999  
R;Ravetch, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H  
Science 234, 718-725, 1986  
A;Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc  
A;Reference number: S29360; MUID:87042761; PMID:2946078  
A;Accession: S29360  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-261 <RAV>  
A;Cross-references: EMBL:M14215; NID:G193247; PIDN:AAA37604.1; PID:G309228  
R;Feilman, R.; Qiu, W.Q.; Pearse, R.N.; Nikolaiczky, B.S.; Sen, R.; Sheffery, M.; Raveto  
EMBO J. 13, 3852-3860, 1994  
A;Title: PU.1 and an HUH family member contribute to the myeloid-specific transcription  
A;Reference number: S46999; MUID:94349933; PMID:8070412  
A;Accession: S46999  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-22 <FEI>  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: immunoglobulin receptor; transmembrane protein  
F;130-183/Domain: immunoglobulin homology <IMM>  
  
Query Match 30.7%; Score 387.5; DB 2; Length 261;  
Best Local Similarity 35.7%; Pred. No. 2.4e-23;  
Matches 84; Conservative 43; Mismatches 93; Indels 15; Gaps 5;  
  
QY 4 KPQKSLNPPNRIKGENVTLTCNGNNFFVSVSTKWFHNGSLSSEETNSLSINIVNAKFED 62  
DB 34 KAVKLDPPMIQVLKEDNVTLMCEGHNPGNSSTQWFHNGRSRSQVQASYTE-KATVND 92  
  
QY 63 SGKYKQHQVNESEPVYLEVFDWLLQASAEVWMEGQPLFLRCHGWRNWDVYKVIYK 122  
DB 93 SGYRCQMEQRLSDPVDLQVSDWLLQTPQVFLEGETITLRCHSWRNKLNRISEFFH 152  
  
QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV---IKAPREKYW 178  
DB 153 NEXSVRYHYKNSFIPKANSHSGDYCKGSGSTQHQSKPVTITVQDPATTSSISLVW 212  
  
QY 179 LQFFIPLLVILFAVDTLGLFISTQQVTFLLKIRTRKGRF---LNLNPHKPNPK 230  
DB 213 YHTAFSLVMCLLFAVDTLGLFYVRR-----NLQTPREYKWSLSIRKHQAPQDK 261  
  
RESULT 10  
I46021  
Fc-gamma receptor II - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 23-Jul-1999  
C;Accession: I46021; S40204  
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.  
Immunogenetics 39, 423-427, 1994  
A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.  
A;Reference number: I46021; MUID:94245284; PMID:8198320  
A;Accession: I46021  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-296 <ZHA>  
A;Cross-references: EMBL:X75671; NID:G437978; PIDN:CAA53367.1; PID:G437979  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: immunoglobulin receptor

Query Match 30.1%; Score 381; DB 2; Length 296;  
Best Local Similarity 41.2%; Pred. No. 9.1e-23;  
Matches 70; Conservative 33; Mismatches 65; Indels 2; Gaps 1;  
  
QY 2 POKPK--VSLNPPNRIKGENVTLTCNGNNFFVSVSTKWFHNGSLSSEETNSLSINIVNAK 59  
DB 44 PDLKAVVTICPAMINVLREHVTILTCGTSTFSAGNLTTFHNGSSHTTQKPSYSPRAG 103  
  
QY 60 FEDSGYKQHQVNESEPVYLEVFDWLLQASAEVWMEGQPLFLRCHGWRNWDVYKVI 119  
DB 104 SNDSGYSRCOREQTSLSDFVLDVSDWLLQTPSLVFQEGEINLRCHSWRNQPLNKIT 163

QY 120 YYKDEALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV 169  
DB 164 FYQDKSKIFSYQRTNFSIPRANLSHSGYHCTAFIGKMLHSSQPVNITV 213  
  
RESULT 11  
I72882  
Fc gamma receptor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
C;Accession: I72882  
R;Sears, D.  
J. Immunol. 150, 4364-4375, 1993  
A;Title: Rat Class III Fc gamma receptor isoforms differ in IgG subclass-binding speci  
A;Reference number: I56166; MUID:93246650; PMID:8482840  
A;Accession: I72882  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-267 <RES>  
A;Cross-references: GB:L08446; NID:G204120; PIDN:AAA41151.1; PID:G204121  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: immunoglobulin receptor  
F;55-106/Domain: immunoglobulin homology <IMM>  
  
Query Match 29.7%; Score 375; DB 2; Length 267;  
Best Local Similarity 36.9%; Pred. No. 2.4e-22;  
Matches 76; Conservative 42; Mismatches 84; Indels 4; Gaps 1;  
  
QY 4 KPQKSLNPPNRIKGENVTLTCNGNNFFVSVSTKWFHNGSLSSEETNSLSINIVNAKFEDS 63  
DB 40 KAVKLDPPMIQVLKEDNVTILTCGHNPGNSSTQWFHNGRSRSQVQASYTEKATVND 99  
  
QY 64 SGKYKQHQVNESEPVYLEVFDWLLQASAEVWMEGQPLFLRCHGWRNWDVYKVIYK 123  
DB 100 GYRCMAFTSLSDPVLHLEVISDWLLQTPQVFLEGERITLRCHGWKSIQLARISFLON 159  
  
QY 124 GEAALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV---IKAPREKYWL 179  
DB 160 GFVFSFHPYNSYSLSNANSHSGDYCKAYLGRTEHVSKVTTITVQGSATATSSSLWVF 219  
  
QY 180 QFFIPLLVILFAVDTLGLFISTQQQV 205  
DB 220 HAAFLVLMCLLFAVDTLGLFYVRRNL 245  
  
RESULT 12  
A41357  
Fc gamma (IgG) receptor I (high affinity) form b - human  
N;Alternate names: CD64  
C;Species: Homo sapiens (man)  
C;Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 21-Jan-2000  
C;Accession: A41357; S03019  
R;Allen, J.M.; Seed, B.  
Science 243, 378-381, 1989  
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary  
A;Reference number: A41357; MUID:89100284; PMID:2911749  
A;Accession: A41357  
A;Molecule type: mRNA  
A;Residues: 1-344 <ALL>  
A;Cross-references: GB:X14355; GB:M21090; NID:G31333; PIDN:CAA32536.1; PID:G31334  
R;Allen, J.M.; Seed, B.  
Nucleic Acids Res. 16, 11824, 1988  
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc  
A;Reference number: S03018; MUID:89098339; PMID:2974947  
A;Accession: S03019  
A;Molecule type: mRNA  
A;Residues: 1-344 <ALL>  
A;Cross-references: EMBL:X14355; NID:G31333; PIDN:CAA32536.1; PID:G31334  
A;Note: the authors translated the codon ACT for residue 25 as Ala  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein  
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 29.4%; Score 371.5; DB 2; Length 344;  
 Best Local Similarity 41.0%; Pred. No. 6e-22;  
 Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWRIFKGENVTLCNGNFFVSSSTKWFHNGSLSEBTSSNLINVAKPEDS 63  
 DB 21 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQSTPSYRITSASVND 80  
 QY 64 GEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIYKD 123  
 DB 81 GEYRCQGLSGRSDPIQLIEHREGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 140

QY 124 GEALKYWHYENHISITNATVEDSGTYCTGKWQLDYSEPLNITV 169  
 DB 141 GKAFKFFHNSNLITKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 13

A39878  
 Fc gamma (IgG) receptor I-A (high affinity) precursor - human  
 N:Alternate names: CD64  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Dec-1991 #sequence revision 06-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: A39878; J0304; B41357; S03018; I57525  
 R:van de Winkel, J.G.J.; Ernst, L.K.; Anderson, C.L.; Chiu, I.M.  
 J. Biol. Chem. 266, 13449-13455, 1991  
 A:Title: Gene organization of the human high affinity receptor for IgG, Fc gammaRI (CD64)  
 A:Reference number: A39878; MUID:91302383; PMID:1830050  
 A:Accession: A39878  
 A:Molecule type: DNA  
 A:Residues: 1-374 <V>  
 A:Cross-references: GB:M63830; GB:M63835; NID:g180277; PIDN:AAA35678.1; PID:g180279  
 R:Porces, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.  
 J. Clin. Invest. 90, 2102-2109, 1992  
 A:Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.  
 A:Reference number: 155577; MUID:93055454; PMID:1430234  
 A:Accession: I70304  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-374 <RES>  
 A:Cross-references: GB:L03418; NID:g184840; PIDN:AAA36049.1; PID:g292169  
 R:Allen, J.M.; Seed, B.  
 Science 243, 378-381, 1989  
 A:Title: Isolation and expression of functional high-affinity Fc receptor complementary  
 A:Reference number: A41357; MUID:89100284; PMID:2911749  
 A:Accession: B41357  
 A:Molecule type: mRNA  
 A:Residues: 1-24, 'S', '26-337, 'T', '339-374 <AL1>  
 A:Cross-references: GB:X14356; GB:M21091; NID:g31331; PIDN:CAA32537.1; PID:g31332  
 R:Allen, J.M.; Seed, B.  
 Nucleic Acids Res. 16, 11824, 1988  
 A:Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR  
 A:Reference number: S03018; MUID:89098339; PMID:2974947  
 A:Accession: S03018  
 A:Molecule type: mRNA  
 A:Residues: 1-24, 'S', '26-337, 'T', '339-374 <AL2>  
 A:Cross-references: GB:X14356; NID:g31331; PIDN:CAA32537.1; PID:g31332  
 R:Perez, C.; Wietzerbin, J.; Benech, P.D.  
 Mol. Cell. Biol. 13, 2182-2192, 1993  
 A:Title: Two cis-DNA elements involved in myeloid-cell-specific expression and gamma int  
 ism.  
 A:Reference number: I57525; MUID:93204964; PMID:8455606  
 A:Accession: I57525  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-8 <RE2>  
 A:Cross-references: GB:S57204; NID:g298692; PIDN:AAD13887.1; PID:g4261587  
 C:Genetics:  
 A:Gene: GDB:FCGRIA; CD64  
 A:Cross-references: GDB:I35911; OMIM:146760  
 A:Map position: 1q21-1q21  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology

C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:16-292/Domain: extracellular #status predicted <EXT>  
 F:117-170/Domain: immunoglobulin homology <IMM2>  
 F:293-313/Domain: transmembrane #status predicted <TM>  
 F:59,78,152,159,163,195,240/Binding site: carboxydrate (Asn) (covalent) #status predicte

Query Match 29.4%; Score 371.5; DB 1; Length 374;  
 Best Local Similarity 41.0%; Pred. No. 6.e-22;  
 Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWRIFKGENVTLCNGNFFVSSSTKWFHNGSLSEBTSSNLINVAKPEDS 63  
 DB 21 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQSTPSYRITSASVND 80  
 QY 64 GEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIYKD 123  
 DB 81 GEYRCQGLSGRSDPIQLIEHREGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 140

QY 124 GEALKYWHYENHISITNATVEDSGTYCTGKWQLDYSEPLNITV 169  
 DB 141 GKAFKFFHNSNLITKTNISHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 14

I48471  
 Fc gamma (IgG) receptor high affinity - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text\_change 21-Jan-2000  
 C:Accession: I48471  
 R:Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff  
 Science 260, 695-698, 1993  
 A:Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig  
 A:Reference number: I48471; MUID:93242399; PMID:8480181  
 A:Accession: I48471  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-336 <RES>  
 A:Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor  
 F:128-180/Domain: immunoglobulin homology <IMM>

Query Match 29.2%; Score 369; DB 2; Length 336;  
 Best Local Similarity 38.8%; Pred. No. 9.2e-22;  
 Matches 85; Conservative 40; Mismatches 82; Indels 12; Gaps 6;

QY 4 KPKVSLNPPWRIFKGENVTLCNGNFFVSSSTKWFHNGSLSEBTSSNLINVAKPEDS 63  
 DB 31 KAVITLQPPWVSVOEETVTLHCEVHLHPGSSSTQWFLNGTATQSTPSYRITSASVND 90  
 QY 64 GEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNMDVYKVIYK 122  
 DB 91 GEYRCQGLSGRSDPIQLIEHREGWLLQVSSRVFTEGEPLALRCHAWKDKLVYVLYRN 150

QY 123 GEALKYWHYENHISITNATVEDSGTYCTGKWQLDYSEPLNITV KAPREKXWQFF 182  
 DB 151 NGKSPKF-SGSKIAITLNLSHSIVHCSG-MGRHRYTSAGISITVKAFFLE---LFT 204

QY 183 TPLA-VVILFAVDGTLFSTQQQVTFILKIKRTRKGPRL 220  
 DB 205 TPVLRASVSPFPGSLVILNCETNLLQ-----RPGQLQ 239

RESULT 15

A46480  
 Fc gamma (IgG) receptor high affinity - mouse  
 N:Alternate names: high affinity IgG receptor  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A46480; A43511  
 R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.  
 J. Immunol. 148, 1570-1575, 1992

A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and  
A;Reference number: A46480; MUID:92166399; PMID:1531670  
A;Accession: A46480  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-404 <OSM>  
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC  
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.  
J. Immunol. 144, 371-378, 1990  
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG  
A;Reference number: A43511; MUID:90111035; PMID:2136886  
A;Accession: A43511  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-404 <SEA>  
A;Cross-references: GB:M31314; NID:G200752; PIDN:AAA40056.1; PID:G200753  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: immunoglobulin receptor; transmembrane protein  
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 29.2%; Score 369; DB 2; Length 404;  
Best Local Similarity 43.4%; Pred. No. 1.1e-21;  
Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;

Qy 4 KPVSINPPNRIKGNVTLTCNGNFFEVSTKWFHNGSLSEETNSLINIVNAKFDS 63  
Db 31 KAVITQPPWVSIFQENVTWCCEGPHLPCDSSIQNFINGTAVQISTPYSIPESFQDS 90  
Qy 64 GEYKCOHQVNESEPVYLEVFSDWLLLOASAEVYMEGQPLFLRCHGWRNDVYKVIYKD 123  
Db 91 GEYRCQIGSSMPSPVQLQIHNDWLLLOASRRVLTEGEPLALRCHGWRNDVYKVIYKD 150  
Qy 124 GEALKYWEHNISITNATVEDSGYYCTGKVVQWQDYSEPLNITY 169  
Db 151 GKSFQF-SSDSEVAILKTNLSHSGIYHCSG-TGRHRYTSAGVSITY 194

Search completed: October 6, 2004, 09:23:42  
Job time : 13.7086 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 7.84149 Seconds  
(without alignments)  
1540.558 Million cell updates/sec

Title: US-10-763-400-6

Perfect score: 1264

Sequence: 1 VPQKPKVSLNPPMNRIFKGE.....RTRKGFRLNPPHKNPKNN 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1264	100.0	257	1 FCEA HUMAN	P12319 homo sapien
2	597.5	46.5	250	1 FCEA MOUSE	P20489 mus musculus
3	576.5	45.6	245	1 FCE1 RAT	P12371 rattus norv
4	413.5	32.7	250	1 FCG3 BOVIN	P79107 bos taurus
5	411.5	32.6	254	1 FCG3 HUMAN	P08637 homo sapien
6	411	32.5	257	1 FCG3_PIG	Q28942 sus scrofa
7	399.5	31.6	233	1 FCG3 HUMAN	P075015 homo sapien
8	390	30.9	267	1 FCG3 RAT	P27645 rattus norv
9	387.5	30.7	261	1 FCG3 MOUSE	P08508 mus musculus
10	381	30.1	296	1 FCG3 BOVIN	Q28110 bos taurus
11	374.5	29.6	374	1 FCG1 HUMAN	P12314 homo sapien
12	370.5	29.3	341	1 FCG3_CAVPO	Q60513 cavia porce
13	369	29.2	404	1 FCG1 MOUSE	P26151 mus musculus
14	363.5	28.8	330	1 FCG2 MOUSE	P08101 mus musculus
15	361.5	28.6	285	1 FCG2 RAT	Q63203 rattus norv
16	345	27.3	310	1 FCGB HUMAN	P31994 homo sapien
17	345	27.3	323	1 FCGC HUMAN	P31995 homo sapien
18	341.5	27.0	316	1 FCGA_PANTR	Q85978 pan troglod
19	328	25.9	317	1 FCG3_HUMAN	P12318 homo sapien
20	327	25.9	157	1 FCE2 RAT	P12840 rattus norv
21	170	13.4	1709	1 SN HUMAN	Q9b222 homo sapien
22	162.5	12.9	1694	1 SN MOUSE	Q62230 mus musculus
23	154	12.2	422	1 K3L1 RAT	P83356 rattus norv
24	144	11.4	432	1 K3L1 MOUSE	P83555 mus musculus
25	137.5	10.9	521	1 CEAL1 MOUSE	P31809 mus musculus
26	136.5	10.8	519	1 ECTO RAT	P16573 rattus norv
27	136	10.8	837	1 NCM2 MOUSE	Q35136 mus musculus
28	129.5	10.2	1302	1 NRG DROME	P20241 drosophila
29	128.5	10.2	344	1 CEAG HUMAN	P40199 homo sapien
30	126	10.0	1240	1 NFAS HUMAN	Q94856 homo sapien
31	123	9.7	1240	1 NFAS MOUSE	Q81013 mus musculus
32	123	9.7	1240	1 NFAS RAT	P97685 rattus norv
33	120.5	9.5	739	1 VCAL1 RAT	P29534 rattus norv

#### ALIGNMENTS

##### RESULT 1

FCEA\_HUMAN

ID FCEA\_HUMAN STANDARD; PRT; 257 AA.

AC P12319;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor

DE (FCER1) (IGE Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).

GN FCER1A OR FCER1A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=89233953; PubMed=2967464;

RA Kochan J., Pettine L.F., Hakim J., Kishi K., Kinet J.-P.;

RT "Isolation of the gene coding for the alpha subunit of the human high

RT affinity Ige receptor."

RL Nucleic Acids Res. 16:3584-3584(1988).

RN [2]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Mast cells;

RX MEDLINE=89158102; PubMed=2964640;

RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,

RA Leder P.;

RT "Human and rat mast cell high-affinity immunoglobulin E receptors:

RT characterization of putative alpha-chain gene products.";

Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).

RN [3]

3D-STRUCTURE MODELING OF 26-137.

RX MEDLINE=93113350; PubMed=1472946;

RA Padlan E.A., Helm B.A.;

RT "A modeling study of the alpha-subunit of human high-affinity

RT receptor for immunoglobulin-E.";

RL Receptor 2:1129-144(1992).

CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH

CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC

CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL

CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)

CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR

CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.

CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO

CC DISULFIDE LINKED GAMMA CHAINS.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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CC

DR EMBL; X06948; CAA30025.1; -;  
 DR EMBL; J03605; AAA36204.1; -;  
 DR EMBL; A21606; CAA01564.1; -;  
 DR PIR; S00682; S00682.  
 DR PDB; 1ALS; 27-FEB-95.  
 DR PDB; 1ALT; 27-FEB-95.  
 DR PDB; 1F2Q; 08-JUN-00.  
 DR PDB; 1J86; 29-AUG-01.  
 DR PDB; 1J87; 29-AUG-01.  
 DR PDB; 1J88; 29-AUG-01.  
 DR PDB; 1J89; 05-SEP-01.  
 DR Genew; HGNC:3609; FCERIA.  
 DR MIM; 147140; -.  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00408; IgC2; 1.  
 DR PROSITE; PS50835; IG-Like; 2.  
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; 3D-structure.  
 FT SIGNAL 1 25  
 FT CHAIN 26 257  
 FT DOMAIN 26 205  
 FT TRANSMEM 206 224  
 FT DOMAIN 225 257  
 FT DOMAIN 30 110  
 FT DOMAIN 111 193  
 FT DISULFID 51 93  
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 FT CARBOHYD 191 191  
 FT STRAND 31 35  
 FT HELIX 39 43  
 FT TURN 43 43  
 FT STRAND 48 54  
 FT STRAND 61 66  
 FT TURN 67 68  
 FT STRAND 69 71  
 FT TURN 74 74  
 FT TURN 75 76  
 FT STRAND 77 79  
 FT HELIX 82 87  
 FT STRAND 91 96  
 FT HELIX 98 100  
 FT TURN 101 101  
 FT STRAND 104 107  
 FT STRAND 114 116  
 FT HELIX 120 124  
 FT STRAND 128 133  
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 FT STRAND 175 178  
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 FT STRAND 190 193  
 SQ SEQUENCE 257 AA; 29596 MW; F183B2357DDAD58 CRC64;  
 Query Match 100.0%; Score 1264; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 6.3e-99;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VFQKPKVSLNPPNRI FKGVNVLTCNGNPFVSVSTKWFHNGSLSEETNSLAINAKF 60  
 DB 26 VFQKPKVSLNPPNRI FKGVNVLTCNGNPFVSVSTKWFHNGSLSEETNSLAINAKF 85  
 QY 61 EDSEYKCHQOQVNESEPVYLEVFSDFWLLQASAEVYVNEGOPFLFURCHGWRNDVYKVIY 120  
 DB 86 EDSEYKCHQOQVNESEPVYLEVFSDFWLLQASAEVYVNEGOPFLFURCHGWRNDVYKVIY 145  
 QY 121 YKDGALKYVYENHNISITNATVDSGYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 180  
 DB 146 YKDGALKYVYENHNISITNATVDSGYCTGKVMQLDYSEPLNITVIKAPREKYWLQ 205  
 QY 181 FFIPLLVILFAVDTGFLFISTQQQVTFLLKIKRTRKGRLLNPHPKPNKN 232  
 DB 206 FFIPLLVILFAVDTGFLFISTQQQVTFLLKIKRTRKGRLLNPHPKPNKN 257  
 RESULT 2  
 FCEA\_MOUSE  
 ID FCEA\_MOUSE STANDARD; PRT; 250 AA.  
 AC P20489;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor  
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).  
 GN FCERIA OR FCERIA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89359361; PubMed=2527850;  
 RA Ra C., Jouvin M.H.E., Kinet J.-P.;  
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc epsilon RI) and surface expression of chimeric receptors (rat-mouse-human) on transfected cells.";  
 RL J. Biol. Chem. 264:15323-15327(1989).  
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE) RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES  
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMMA CHAINS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.  
 CC -----  
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 CC -----  
 CC EMBL; J05018; AAA37600.1; -;  
 DR PIR; A34342; A34342.  
 DR HSSP; P12319; 1ALS.  
 DR MGD; MGI:95494; FcERIA.  
 DR GO; GO:0007165; P: signal transduction; IDA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; Ig; 2.  
 DR PROSITE; PS50835; IG-Like; 1.  
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat.

```

FT SIGNAL 1 23 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT CHAIN 24 250 RECEPTOR ALPHA-SUBUNIT.
FT DOMAIN 24 204 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 250 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 104 IG-LIKE 1.
FT DOMAIN 114 181 IG-LIKE 2.
FT DISULFID 49 92 BY SIMILARITY.
FT DISULFID 131 174 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BFB4DC0C4E CRC64;

Query Match 46.5%; Score 587.5; DB 1; Length 250;
Best Local Similarity 52.3%; Pred. No. 3e-42;
Matches 113; Conservative 43; Mismatches 57; Indels 3; Gaps 3;

QY 3 QKPKVSLNPPNRRIFKGENVTLTCNGNFFEV-SSTKWFHNGSLSEETSSLNINVAKFE 61
DB 26 EKVLTLDPPWIRIFTGEKVTLSYGNHLLQMNSTTKWIHNGTVSEVNSHLVIVSATVQ 95

QY 62 DSSEYKCOHQVNESEPPVLEFSDMLLOASAEVMEGQPLRCHGWRNDVYKVIY 121
DB 86 DSKYICQKQGLPKRPVYLVNTQDMLLQTSADMILVHGSPDIRCHGKNWVRKVIY 145

QY 122 KDGEALKYWHNNHISITNATVDSGTYYCTGKQWQDYSEPLNITVIKAPREK-YWLO 180
DB 146 RNDHAFNYSYES-PVSIREATLNSDGYHCKGYLRQVEYSDKFRIAVAVKAYCKYWLQ 204

QY 181 FTFPLLVILFAVDTGFISTQQQVTFLLKIKSTRK 216
DB 205 LIFPLLVAIFAVDTGTLTSTEEQKSVLEIQTKG 240

RESULT 3
FCE1_RAT STANDARD; PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCER1) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
DE GN FCER1A OR FCE1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakimi J., Kochan J.;
RT "A cDNA presumptively coding for the alpha subunit of the receptor
RT with high affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RN [2]
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Test cells;
RX MEDLINE=88158102; PubMed=2264640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).

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(4)
RN SEQUENCE OF 21-245 FROM N.A.
RP MEDLINE=88289772; PubMed=2969594;
RX Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity Ige receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC !- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LIPIDOKINES.
CC !- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC !- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC !- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC
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CC
CC EMBL; M17153; AAA42045.1; -
CC EMBL; J03606; AAA41582.1; -
CC EMBL; M21622; AAA41146.1; -
CC PIR; C31327; A30154.
CC HSP; F12319; 1AUS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC Pfam; PF00047; IG; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS00835; IG LIKE; 1.
KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 245 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT DOMAIN 24 204 RECEPTOR ALPHA-SUBUNIT.
FT TRANSMEM 205 223 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 224 245 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 103 IG-LIKE 1.
FT DOMAIN 113 181 IG-LIKE 2.
FT DISULFID 49 91 BY SIMILARITY.
FT DISULFID 130 174 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 245 AA; 27793 MW; A0B67DD363B72197 CRC64;

Query Match 45.6%; Score 576.5; DB 1; Length 245;
Best Local Similarity 51.4%; Pred. No. 2.5e-41;
Matches 111; Conservative 39; Mismatches 65; Indels 1; Gaps 1;

QY 3 QKPKVSLNPPNRRIFKGENVTLTCNGNFFEV-SSTKWFHNGSLSEETSSLNINVAKPED 62
DB 26 QKSVSLDPPWIRILTGDVTLICNGNSSQVNTKWIHNDISINVKSSHVIVSATIQD 85

QY 63 SGEYKCOHQVNESEPPVLEFSDMLLOASAEVMEGQPLRCHGWRNDVYKVIYK 122
DB 86 SGKYICQKQGYKSPVYLVNTQDMLLQTSADMILVHGSPDIRCHGKNWVRKVIYK 145

QY 123 DGEALKYWHNNHISITNATVDSGTYYCTGKQWQDYSEPLNITVIKAPREKY-WLOF 181
DB 146 DDIAFKYSDSNISIRKATFNDSGSYHCTGYLNKVECKDFESIAVVDYTIERYWLQ 205

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QY 182 FPLLLVILFAVDTLGLFISTQQQVTLFLKIKETKRG 217  
 DB 206 IFPSLAVILFAVDTLGLFWSTHKGQFESILKIKGTGK 241

RESULT 4  
 ID FCG3 BOVIN STANDARD; PRT; 250 AA.  
 AC 279107;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region precursor  
 DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).  
 GN FCGR3 OR FCGRIII.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph node;  
 RX MEDLINE=97246739; PubMed=9089104;  
 RA Collins R.A., Gelder K.I., Howard C.J.;  
 RT "Nucleotide sequence of cattle FCGRIII: its identification in  
 gamma delta T cells.";  
 RL Immunogenetics 45:440-443(1997).  
 CC -!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED  
 CC OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-  
 CC DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT  
 CC ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; X99695; CRA68026.1; -.  
 DR HSSP; P12319; 1ALS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 2.  
 DR PROSITE; PS50835; IG-LIKE; 2.  
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW immunoglobulin domain; Repeat; Polymorphism.  
 FT SIGNAL 1 16  
 FT CHAIN 17 250  
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 FT REGION RECEPTOR III.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 209 225  
 FT INTRACELLULAR (POTENTIAL).  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE 1.  
 FT IG-LIKE C2-TYPE 2.  
 FT BY SIMILARITY.  
 FT DISULFID 47 89  
 FT BY SIMILARITY.  
 FT DISULFID 128 172  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 56 56  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 63 63  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 180 180  
 FT P -> L.  
 FT V -> L.  
 FT VARIANT 11 11  
 FT VARIANT 12 12  
 FT VARIANT 46 46  
 FT VARIANT 107 107  
 FT VARIANT 114 114  
 FT VARIANT 229 229  
 FT V -> I.  
 SQ SEQUENCE 250 AA; 28050 MW; DE625139E889E207 CRC64;

Query Match 32.7%; Score 413.5; DB 1; Length 250;  
 Best Local Similarity 40.8%; Pred. No. 1.2e-27;  
 Matches 86; Conservative 35; Mismatches 82; Indels 9; Gaps 2;

QY 2 POKPKVSLNPPNRIKGENVTILTCNNGNFFVSTTKWFHNGSLSEETNSSLNIVNAKPE 61  
 DB 23 PSKAVLLDPQNNHVLNDRVTLKCGDYVPEDNSTKWHNGTLISSQTPSYFIADVKVQ 82  
 QY 62 DSGEYKQHQVNESEPVLEVFSFVLLQAAEAVVMGQPLFLRCHGWNRWDVVKVIY 121  
 DB 83 DSGEYKQGLSAPSPPVLEVEVGLLQAAQVNVVGVKPIRLKCHSWKTKTFVAKVQF 142  
 QY 122 KDGEALKYWEHNHNSITNATVEDSTGYCTCKWQLDVSEPLNITVTKAPREKVMQF 181  
 DB 143 RNRGRKKYSHGNSDFHIPEAKLEHSGSVFCRIIGSKESSESVOITV-QAPETLQTVSS 201  
 QY 182 FIP-----LLWILFAVDTLGLFISTQQQV 205  
 DB 202 FFPFPHQITFCLVMGVLFVAVDTGLYFSVRRHL 233

RESULT 5  
 FC3A\_HUMAN STANDARD; PRT; 254 AA.  
 ID FC3A\_HUMAN  
 AC P08637;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor  
 DE (IGG Fc receptor III-2) (Fc-gamma RIII-alpha) (Fc-gamma RIIIA)  
 DE (FCRIIA) (FC-gamma RIII) (FCRIII) (CD16-A) (FCR-10).  
 GN FCGR3A OR FCGR3 OR FCGR3 OR IGR3 OR CD16A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89328325; PubMed=2526846;  
 RX Ravetch J.V., Petrusia B.;  
 RA "Alternative membrane forms of Fc gamma RIII (CD16) on human natural  
 RT killer cells and neutrophils. Cell type-specific expression of two  
 RT genes that differ in single nucleotide substitutions.";  
 RL J. Exp. Med. 170:481-497(1989).  
 RN [2]  
 RP SEQUENCE OF 1-39 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=95138131; PubMed=7836402;  
 RA Gessner J.E., Grussermeyer T., Kolarus W., Schmidt R.E.;  
 RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B  
 RT genes. Molecular characterization of the promoter regions.";  
 RL J. Biol. Chem. 270:1350-1361(1995).  
 RN [3]  
 RP VARIANTS ARG-66 AND HIS-66.  
 RX MEDLINE=96183251; PubMed=8609432;  
 RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,  
 RA van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;  
 RT "A triallelic Fc gamma receptor type IIA polymorphism influences the  
 RT binding of human IGG by NK cell Fc gamma RIIIA.";  
 RL J. Immunol. 156:3948-3955(1996).  
 RN [4]  
 RP VARIANT VAL-157.  
 RX MEDLINE=97385047; PubMed=9242542;  
 RA Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,  
 RA de Haas M.;  
 RT "Fc gammaRIIA-158V/F polymorphism influences the binding of IgG by  
 RT natural killer cell Fc gammaRIIA, independently of the Fc  
 RL gammaRIIA-48L/R/H phenotype.";  
 RL Blood 90:1109-1114 (1997).  
 RN [5]  
 RP VARIANT VAL-176.  
 RX MEDLINE=97428467; PubMed=9276722;  
 RA Wu J., Edberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,



Salmon J.E., Kimberly R.P.;  
"A novel polymorphism of FcgammaRIIIa (CD16) alters receptor function  
and predisposes to autoimmune disease.";  
J. Clin. Invest. 100:1059-1070(1997).  
-- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG.- BINDS COMPLEXED OR  
CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT  
RESPONSES, SUCH AS PHAGOCYTOSIS.  
-- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC  
EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.  
-- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists  
also as a soluble receptor.  
-- TISSUE SPECIFICITY: Expressed on natural killer cells,  
macrophages, subpopulation of T cells, immature thymocytes and  
placental trophoblasts.  
-- PTM: Glycosylated. Contains high mannose- and complex-type  
oligosaccharides.  
-- PTM: The soluble form is produced by a proteolytic cleavage.  
-- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of  
IgG1, IgG3 and IgG4 compared with isoform Phe-157. Alleles Leu-66  
and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in  
linkage disequilibrium.  
-- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:  
FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-  
SPECIFIC MANNER. THE SER-203 IN III-A DETERMINES THE TRANSMEMBRANE  
DOMAINS WHEREAS THE PER-203 IN III-B DETERMINES THE GPI-ANCHORING.  
-- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
-- DATABASE: NAME=PROW; NOTE=CD guide CD16a entry;  
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdl6a.htm".

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EMBL; X52645; CAAC36870.1; --  
EMBL; Z46222; CAAB6295.1; --  
FIR; JL0107; JL0107.  
HSPR; PL2319; IALS.  
Genev; HGNC:3619; FCGR3A.  
MIM; 146740; --  
GO; GO:0005886; C:plasma membrane; TAS.  
GO; GO:006955; P:immune response; TAS.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003599; Ig.  
Pfam; PF00047; IG; 2.  
SMART; SMO0409; IG; 2.  
DR PROSITE; PS50835; IG LIKE; 2.  
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Immunoglobulin domain; Repeat; Multigene family; Polymorphism.

SIGNAL 1 16  
CHAIN 17 254  
FT FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
FT FT POTENTIAL.  
FT FT LEU AFFINITY RECEPTOR III-A.  
FT FT EXTRACELLULAR (POTENTIAL).  
FT FT TRANSMEM .  
FT FT POTENTIAL.  
FT FT CYTOPLASMIC (POTENTIAL).  
FT FT IG-LIKE C2-TYPE 1.  
FT FT IG-LIKE C2-TYPE 2.  
FT FT BY SIMILARITY.  
FT FT BY SIMILARITY.  
FT FT N-LINKED GLCNAC. . ) (POTENTIAL).  
FT FT N-LINKED GLCNAC. . ) (POTENTIAL).  
FT FT N-LINKED GLCNAC. . ) (POTENTIAL).  
FT FT N-LINKED GLCNAC. . ) (POTENTIAL).  
FT FT CARBOHYD 180 180  
FT FT CARBOHYD 187 187  
FT FT VARIANT 66 66 L -> R  
FT FT /FTId=VAR\_008799.  
FT FT L -> H.  
FT FT /FTId=VAR\_008800.  
FT FT F -> V.  
FT FT VARIANT 157 157

```

FT FTID=VAR_008801.
FT F > V (in dbSNP:396991).
FT /FTID=VAR_003960.
FT FT SEQUENCE 254 AA; 29089 MW; D38D179D32C67337 CR C64;
SQ
Query Match 32.6%; Score 411.5; DB 1; Length 254;
Best Local Similarity 41.6%; Pred. No. 1.7e-27;
Matches 87; Conservative 33; Mismatches 82; Indels 7; Gaps 1;

QY 4 KPKVSLNPWNRIKFGENTVLTICNGNPFVSTKWFHNGSLSEETNSSLIYNVAKFEFS 63
Db 25 KAVVLEPQWRYVLEKDSVTLKCGAYSPEDNSTOWFHNESLISQASSYFDAAVDDSS 84
QY 64 GEYKCOHQQWNESEPVYLVESDWLLQLQASAEVVMGQPLFLFCHGWRWMDVYKVYYKD 123
Db 85 GEYRCOTNLTSLSDPVLQEVHGWIGWLLQLQAPRWVFKEDPIHLRCHSKWNTALHKVTYLN 144
QY 124 GEALKRYWENHNISITNATVEDSGTYCYCKWQWLDYSEPLNITVIKAPREKVVLOFFI 183
Db 145 GKGRKVFHNSDFYIPKATLKDSGYSFCRGLFGSKVSVETNITITQGLAVSTISSFFP 200
QY 184 P-----LLVILFAVDTCFLFISTQQOV 205
Db 205 PGYQVSFCLVWLLFAVDTCGLYFSVKTN 233

RESULT 6
FCG3_PIG STANDARD; PRT; 257 AA.
ID FCG3_PIG STANDARD; PRT; 257 AA.
AC Q28942; Q28940; Q28941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII) (Cytolytic trigger
DE molecule G7).
DE FCGR3.
GS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
RX STRAIN=Mannesota miniature swine;
RX MEDLINE=94358430; PubMed=8077673;
RA Halloran P.J., Sweeney S.E., Strohmaier C.M., Kim Y.B.;
RT "Molecular cloning and identification of the porcine cytolytic
RT trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue.";
RL J. Immunol. 153:2631-2641(1994).
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC -!- SUBUNIT: FORMS A COMPLEX WITH NK-E.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PBMC,
CC MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
CC THYMUS OR LIVER.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; U08993; AAA57190.1; -
CC EMBL; U08991; AAA57188.1; -
CC EMBL; U08992; AAA57189.1; -
CC HSSP; F12319; 1ALS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.

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CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD16B entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd16b.htm".  
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 CC  
 CC ENBL; X16863; CAA34753.1; -;  
 CC DR ENBL; X07934; CAA30758.1; -;  
 CC DR ENBL; J04162; AAA35881.1; -;  
 CC DR ENBL; Z46223; CAA86296.1; -;  
 CC DR PIR; J0284; J0284;  
 CC DR PDB; 1E4J; 04-AUG-00.  
 CC DR PDB; 1E4K; 06-JUN-01.  
 CC DR PDB; 1FNU; 22-NOV-00.  
 CC DR PDB; 1IIS; 16-MAY-01.  
 CC DR PDB; 1IIX; 16-MAY-01.  
 CC DR Genew; HGNC:3620; FCGR3B.  
 CC GO; GO:0006955; P:Immune response; TAS.  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003599; Ig.  
 CC DR Pfam; PF00047; Ig; 2.  
 CC DR SMART; SM00409; Ig; 2.  
 CC DR PROSITE; PSS0835; Ig-Like; 1.  
 CC DR IgG-binding protein; Receptor; GPI-anchor; Glycoprotein; Signal;  
 CC KW Immunoglobulin domain; Repeat; Multigene family; Polymorphism;  
 CC KW 3D-structure; Lipoprotein.  
 CC FT SIGNAL 1 16  
 CC FT CHAIN 17 200  
 CC  
 CC PROPEP 201 233  
 CC FT LIPID 200 200  
 CC FT DOMAIN 40 96  
 CC FT DOMAIN 121 179  
 CC FT DISULFID 47 89  
 CC FT DISULFID 128 172  
 CC FT CARBOHYD 56 56  
 CC FT CARBOHYD 63 63  
 CC FT CARBOHYD 82 82  
 CC FT CARBOHYD 92 92  
 CC FT CARBOHYD 180 180  
 CC FT CARBOHYD 187 187  
 CC FT VARIANT 36 36  
 CC  
 CC FT VARIANT 65 65  
 CC FT VARIANT 78 78  
 CC FT VARIANT 82 82  
 CC FT VARIANT 106 106  
 CC FT SEQUENCE 233 AA; 26216 MW; 7AB5159432761726 CRC64;  
 CC  
 CC Query Match 31.6%; Score 399.5; DB 1; Length 233;  
 CC Best Local Similarity 41.1%; Pred. No. 1.6e-26;  
 CC Matches 86; Conservative 32; Mismatches 84; Indels 7; Gaps 1;  
 CC  
 CC 4 KPKVSLNPPWNRIFKGVNLTTCNGNFFVSSYTKWFGSLSBETNSLSLVNAKPEDS 63  
 CC 25 KAVVLEQWYSVLEKDSVTLKCGAYSPEDNQCWFPHNESLISSQASSYFIDAATVND 84  
 CC 64 GYKCOHQVNESEPVYLEVSDWLLLOASAEVWMEGQPLRCHGWENWVYKVIYKD 123  
 CC 85 GEYRCQTNLSTLSDVQLVHIGWLLQAPRWVFEEDPIHLRCHSWKNTALHKVYLQN 144  
 CC 124 GEALXVYENHNISITNATVEDSGTYCTGKVMQDYSEPLNITVIKAPREKYWLPFI 183

Db 145 GKDRKYPFHNSDFHIPKATLKDSSYFCRGLVSGKNVSSVTVNITITQGLAVSTISSFSP 204  
 QY 184 P-----LLVWVILFAVDITGLFISTQOQV 205  
 Db 205 PGYQVSCLVNVLFAVDITGLYFSVKINI 233  
 RESULT 8  
 FCGR3 RAT STANDARD; PRT; 267 AA.  
 ID FCGR3 RAT PRT; 267 AA.  
 AC P27645; Q04798; Q63204;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor  
 DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).  
 GN FCGR3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM B; C AND D).  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=91250730; PubMed=1710249;  
 RA Farber D.L., Sears D.W.;  
 RT "Rat CD16 is defined by a family of class III Fc gamma receptors  
 RT requiring co-expression of heteroprotein subunits.";  
 RL J. Immunol. 146:4352-4361(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=Natural killer cells;  
 RX MEDLINE=90239026; PubMed=1692135;  
 RA Zeger D.L., Hogarth P.M., Sears D.W.;  
 RT "Characterization and expression of an Fc gamma receptor cDNA cloned  
 RT from rat natural killer cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM H).  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=93246650; PubMed=8482840;  
 RA Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P.,  
 RA Sears D.W.;  
 RT "Rat class III Fc gamma receptor isoforms differ in IgG subclass-  
 RT binding specificity and fail to associate productively with rat CD3  
 RT zeta.";  
 RL J. Immunol. 150:4364-4375(1993).  
 CC -1- FUNCTION: Receptor for the Fc region of complexed immunoglobulins  
 CC gamma. Low affinity receptor.  
 CC -1- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS.  
 CC THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE  
 CC EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=C;  
 CC IsoId=P27645-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=P27645-3; Sequence=Not described;  
 CC Name=B;  
 CC IsoId=P27645-4; Sequence=Not described;  
 CC Name=D;  
 CC IsoId=P27645-5; Sequence=Not described;  
 CC Name=E;  
 CC IsoId=P27645-6; Sequence=Not described;  
 CC Name=F;  
 CC IsoId=P27645-7; Sequence=Not described;  
 CC Name=G;  
 CC IsoId=P27645-8; Sequence=Not described;  
 CC Name=H;  
 CC IsoId=P27645-2; Sequence=VSP\_003647;  
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON NATURAL KILLERS CELLS AND

CC CC MACROPHAGES.  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M64368; AAA42049.1; -  
 CC EMBL; M64369; AAA42048.1; -  
 CC EMBL; M64370; AAA42050.1; -  
 CC EMBL; M32062; AAA41148.1; -  
 CC EMBL; L08446; AAA41151.1; -  
 CC PIR; A35902; A35902.  
 CC PIR; I56110; I56110.  
 CC HSP; P12319; IALS.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003599; Ig.  
 CC Pfam; PF00047; Ig; 2.  
 CC SMART; SM00409; Ig; 2.  
 CC PROSITE; PS50835; IG-LIKE; 2.  
 CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 CC Immunoglobulin domain; Repeat; Alternative splicing.  
 CC SIGNAL 1 36  
 CC CHAIN 37 267  
 CC LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 CC REGION RECEPTOR III.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC IG-LIKE C2-TYPE 1.  
 CC IG-LIKE C2-TYPE 2.  
 CC BY SIMILARITY.  
 CC BY SIMILARITY.  
 CC SWKQKLTQVLLFQNGKPRVYVYSSNFSIPK -> GWKSI  
 CC QLARISFLQNGEFVSHFYNVSISN (in isoform  
 CC H).  
 CC /FTID=VSP\_002647.  
 CC ANLP -> GDL (IN ISOFORM A AND ISOFORM  
 CC H).  
 CC E -> D (IN ISOFORM A AND ISOFORM  
 CC H).  
 CC D -> G (IN ISOFORM D).  
 CC V -> I (IN ISOFORM A AND ISOFORM B).  
 CC E -> L (IN ISOFORM H).  
 CC T -> R (IN ISOFORM H).  
 CC N -> D (IN ISOFORM H).  
 CC M -> E (IN ISOFORM H).  
 CC K -> R (IN ISOFORM H).  
 CC SEQUENCE 267 AA; 30281 MW; DD4DS6A7A3F70ED92 CRC64;  
 CC  
 CC Query Match 30.9%; Score 390; DB 1; Length 267;  
 CC Best Local Similarity 37.9%; Pred. No. 1.2e-25;  
 CC Matches 78; Conservative 40; Mismatches 84; Indels 4; Gaps 1;  
 CC  
 CC QY 4 KPKVSLAPPNNRIFKGENVTITCGNNFFVSSSTKWFHNGSLSEETNSLNIYNAKFE 63  
 CC DB 40 KAVVRDPFWITQVLKEDTITVTCGTHNPGNSSTGQVFNQSSWTGQVQSYTFKATVND 99  
 CC QY 64 GEYKQHQVNESEPVLYEFDVLLQLQASAEVMEQGPLFRCRGWRNDVVKVYVKD 123  
 CC DB 100 GEYCRVAHTSLSPVHLEISDWLLIQTPLQFEEGETITLRCHSKWQLTKVLLFQN 159  
 CC QY 124 GEALKYVENHNSITATVEDSGTYCTKWQLDVSEPLNITV----IKAPREKYWL 179  
 CC DB 160 GKPVRYVYQSNFSIPKANHSHSGNYYCKAYLGRTHVSRKPVITVQGSATASSTSLVWF 219  
 CC QY 180 QFFPLLVILFAVDITGLFISTQQCV 205.  
 CC DB 220 HAAFLVACLLFAVDITGLYFCVRNL 245

RESULT 9  
 FC3\_MOUSE  
 ID FC3\_MOUSE STANDARD; PRT; 261 AA.  
 AC P08508; 1988 (Rel. 08, Created).  
 DT 01-AUG-1988 (Rel. 08, Last sequence update).  
 DT 01-AUG-1988 (Rel. 08, Last sequence update).  
 DT 10-OCT-2003 (Rel. 42, Last annotation update).  
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor  
 DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII).  
 GN FCGR3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87042761; PubMed=2946078;  
 RA Ravetch J.V., Luster A.D., Weinshank R., Kochan J., Pavlovic A.,  
 RA Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;  
 RT "Structural heterogeneity and functional domains of murine  
 RT immunoglobulin G Fc receptors.";  
 RL Science 234:718-725(1986).  
 RN [2]  
 RP SEQUENCE OF 1-29 FROM N.A.  
 RC STRAIN=BALB/c; TISSUE=Liver;  
 RA Soares H.J., Onken M.D., Kulczycki A. Jr.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for the Fc region of complexed immunoglobulins  
 CC gamma. Low affinity receptor.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M14215; AAA37604.1; -  
 CC EMBL; X60929; CAA43266.1; -  
 CC PIR; S29360; S29360.  
 CC HSP; P12319; IALS.  
 CC MGD; MGI:95500; Fcgr3.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003599; Ig.  
 CC Pfam; PF00047; Ig; 2.  
 CC SMART; SM00409; Ig; 2.  
 CC PROSITE; PS50835; IG-LIKE; 2.  
 CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 CC Immunoglobulin domain; Repeat.  
 CC SIGNAL 1 30  
 CC CHAIN 31 261  
 CC POTENTIAL.  
 CC LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 CC REGION RECEPTOR III.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC IG-LIKE C2-TYPE 1.  
 CC IG-LIKE C2-TYPE 2.  
 CC BY SIMILARITY.  
 CC BY SIMILARITY.  
 CC N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. .) (POTENTIAL).  
 CC SEQUENCE 261 AA; 30036 MW; 757FB8368E41069 CRC64;  
 CC  
 CC Query Match 30.7%; Score 387.5; DB 1; Length 261;  
 CC Best Local Similarity 35.7%; Pred. No. 1.9e-25;  
 CC Matches 84; Conservative 43; Mismatches 93; Indels 15; Gaps 5;  
 CC  
 CC QY 4 KPKVSLAPPNNRIFKGENVTITCGNNFFVSSSTKWFHNGSLSEETNSLNIYNAKFE 62

[illegible]

RESULT 10	
FCCG2 BOVIN	
ID_FCG2 BOVIN	
STANDARD:	PRT: 296 AA.

AC	Q28110; 01-NOV-1997 (Rel. 35, Created)
AC	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-gamma RII) (FcRII) (IgG Fc receptor II).
DE	FCGR2.
GN	Bos taurus (Bovine).
GN	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OC	NCBI TaxID=9913;
OC	NCBI TaxID=9913;

[1] -	
SEQUENCE FROM N.A.	
MEDLINE=94245284; PubMed=8188320;	
Zhang G., Young J.R., Iregaskes C.R., Howard C.J.;	
"Cattle Fc gamma RI: molecular cloning and ligand specificity.";	
Immunogenetics 39:423-427(1994).	
-!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low	
affinity receptor.	
-!- SUBCELLULAR LOCATION: Type I membrane protein.	
-!- TISSUE SPECIFICITY: Higher expression is found in macrophages than	
in neutrophils (Probable).	
-!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred	
to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).	
This motif is involved in downmodulation of cellular responses.	
The phosphorylated ITIM motif binds to the SH2 domain of	
PTPN6/SHP-1.	

-- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC	EMBL; X75671; CAA53367.1; -.
DR	P1R; I46021; I46021.
DR	HSP; P12319; IALS.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003599; IG.
DR	Pfam; PF00047; IG; 2.
DR	SMART; SM00409; IG; 2.
DR	PROSITE; PS50835; IG LIKE; 2.
KW	IG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW	Immunoglobulin domain; Repeat.
FT	SIGNAL 1 42
FT	CHAIN 43 296
FT	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT	REGION RECEPTOR II.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOPLASMIC (POTENTIAL).

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KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; Alternative splicing; Phosphorylation;  
 KW Polymorphism.  
 FT SIGNAL 1 29  
 FT CHAIN 30 330  
 FT DOMAIN 30 210  
 FT TRANSMEM 211 231  
 FT DOMAIN 232 330  
 FT DOMAIN 50 106  
 FT DOMAIN 131 189  
 FT SITE 307 312  
 FT DISULFID 57 99  
 FT DISULFID 138 182  
 FT CARBOHYD 65 65  
 FT CARBOHYD 92 92  
 FT CARBOHYD 166 166  
 FT CARBOHYD 173 173  
 FT VARSPLIC 243 290  
 FT VARSPLIC 262 290  
 FT VARIAT 116 116  
 FT VARIAT 116 116  
 FT VARIAT 145 145  
 FT VARIAT 161 161  
 FT VARIAT 161 161  
 FT VARIAT 190 190  
 FT VARIAT 195 195  
 FT VARIAT 287 287  
 FT CONFLICT 270 278  
 FT CONFLICT 299 299  
 Query Match 28.8%; Score 363.5; DB 1; Length 330;  
 Best Local Similarity 38.9%; Pred. No. 2.5e-23;  
 Matches 77; Conservative 40; Mismatches 72; Indels 9; Gaps 5;  
 QY 4 KPVSLNPPNRRIFKGENVTLTCGNNGFFVSVSTKWFHNGSLSEBTNSLNIIVNAKFPD 62  
 Db 35 KAVVKLEPPWQVLKEDVTLTCEGTHNPGNSSTQWFHNGSIRSQVASYTF-KATVND 93  
 QY 63 SGKYKCHQOVNESEPVYLEVFDSDLLQASAVVMEGQPLFLRCHGWRNDVYKVIYK 122  
 Db 94 SGKYRCQMEQLSDPVDLGVISDWLLQTPQLVFLGEGTITLRCHSWRNKLLNRSFFH 153  
 QY 123 DGBALKVYENHNISITNATVEDSGTYCTGKWKQDLYSEPLNITVIKAPREKYWLQFF 182  
 Db 154 NEKSVRTHYSSNFSIPKANSHSGDYCKGSLGRTLHQSKPTIIV-QGPKSSRL--- 209  
 QY 183 IPLVLVILFVDTGLFIS 200  
 Db 210 -PVLTIIV--AAVTGIAVA 224  
 RESULT 15  
 FC2 RAT STANDARD; PRT; 285 AA.  
 AC Q63203;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-  
 gamma RII) (FcRII) (IgG Fc receptor II beta).  
 DE FCGR2.  
 GN Rattus norvegicus (Rat).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94009652; PubMed=8405417;  
 RA Bocek P., Pecht I.;  
 RT "Cloning and sequence of the cDNA coding for rat type II Fc gamma  
 receptor of mast cells";  
 RL FEBS Lett. 331:86-90(1993).  
 CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low  
 affinity receptor. By binding to IgG it initiates cellular  
 responses against pathogens and soluble antigens.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred  
 to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).  
 CC This motif is involved in downmodulation of cellular responses.  
 CC The phosphorylated ITIM motif binds to the SH2 domain of  
 FYN6/SH-1.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X73371; CRA51788.1; -.  
 DR PIR; S36903; S36903.  
 DR HSP; F12319; IALS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003599; Ig.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; Ig; 2.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 31  
 FT CHAIN 32 285  
 FT DOMAIN 32 212  
 FT TRANSMEM 213 233  
 FT DOMAIN 234 285  
 FT DOMAIN 36 118  
 FT DOMAIN 119 201  
 FT SITE 262 267  
 FT SITE 59 101  
 FT DISULFID 140 184  
 FT CARBOHYD 67 67  
 FT CARBOHYD 75 75  
 FT CARBOHYD 86 86  
 FT CARBOHYD 94 94  
 FT CARBOHYD 168 168  
 FT CARBOHYD 175 175  
 FT SEQUENCE 285 AA; 32047 MW; 255540A584CFFA0A CRC64;  
 SQ  
 Query Match 28.6%; Score 361.5; DB 1; Length 285;  
 Best Local Similarity 38.2%; Pred. No. 3.1e-23;  
 Matches 71; Conservative 38; Mismatches 72; Indels 5; Gaps 2;  
 QY 4 KPVSLNPPNRRIFKGENVTLTCGNNGFFVSVSTKWFHNGSLSEBTNSLNIIVNAKFPD 63  
 Db 37 KAVVKLEPPWQVLKEDVTLTCEGTHNPKNSSTQWFHNGSSIMHQANVTFFKATVND 96  
 QY 64 SGKYKCHQOVNESEPVYLEVFDSDLLQASAVVMEGQPLFLRCHGWRNDVYKVIYK 123  
 Db 97 SGKYRCMEETGISSEPIHLGVISDWLLQTSQVFEGETITLRCHSWKNKQLTKVLLFQN 156  
 QY 124 GEALXYVYENHNISITNATVEDSGTYCTGKWKQDLYSEPLNITVIKAPREKYWLQFFI 183  
 Db 157 GPKVRYHQSSNFSIPKANSHSGNYKAVLGRTHVSKPTIIV-QEPKSSSL--- 211  
 QY 184 PLLVVI 189  
 Db 212 PVLTIIV 217

Tue Oct 12 09:19:28 2004

us-10-763-400-6.rsp

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Search completed: October 6, 2004, 09:03:37  
Job time : 8.84149 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      October 6, 2004, 08:59:40 ; Search time 36.5035 seconds
              (without alignments)
              2005.293 Million cell updates/sec

Title:
Perfect score: 1264
Sequence:      1 VPQPKVSLNPWNRIKGE.....RTRKGFRLNHPHPXPNKNN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:      1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

## RESULT 1

PRELIMINARY: PRT: 255 AA.

AC	Q8MI30;		Created
DT	01-OCT-2002	(TrEMBLrel. 22,	
DT	01-OCT-2002	(TrEMBLrel. 22,	Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25,	Last annotation update)
DE	with affinity immunoglobulin E receptor alpha subunit.		

OS *Equus caballus* (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

SEQUENCE FROM N.A.  
 STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;  
 MEDLINE=20424522; PubMed=10970105;  
 MCALEESE S.M., HALLIWELL R.E.W., MILLER H.R.P.;  
 "Cloning and Sequencing of the horse and sheep high-affinity Ige  
 receptor alpha chain cDNA";  
 Immunogenetics 51:872-881(2000).

DR EMBL; I18204; CAB#0367.1; .  
DR GO: GO:0004872; E:receptor activity; IEA.  
DR

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro: IPR003336; Ig\_C2.  
DR Pfam: PF00047; Ig: 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS30835; 19 LINE; 2.  
Immunoglobulin domain: Receptor.  
KW

SQ SEQUENCE 255 AA; 29366 MW; A606597006

1000

Query Match	Best Local Similarity	Pred. No. 3:	Score (03:3)
	62.1%	66.2%	

Matches 151; Conservative 29; Mismatches

• COUNTRY INFORMATION T E X C O N T A I N S F R E E

QY 3 QAPKVS LNF FWNKIF NGENV IJICRGHNTL I : : :

db 28 RKSTVSLNPPWNRI FRGENVTLTCKNKNKPLKCG

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	785.5	62.1	255	6	Q8M130	Q8m130 equus caball
2	743	58.8	260	6	Q8MJ20	Q8mj20 ovis aries
3	409.5	32.4	254	6	Q8SPW2	Q8spw2 macaca fasc
4	398.5	31.5	280	4	Q92637	Q92637 homo sapien
5	396	31.3	249	6	Q92616	Q92616 felis silve
6	396	31.3	250	6	Q9N215	Q9n215 felis silve
7	396	31.3	256	6	Q9S232	Q9s232 sus scrofa
8	395.5	31.3	233	4	Q9UP77	Q9up77 homo sapien
9	384.5	30.4	249	11	Q8R477	Q8r477 mus musculu
10	384	30.4	261	11	Q9E392	Q9e392 mus musculu
11	382.5	30.3	249	11	Q8R394	Q8r394 mus musculu
12	376.5	28.8	357	6	Q8SPW5	Q8spw5 macaca fasc
13	372	23.4	261	11	Q7TMW9	Q7tmw9 mus musculu
14	371.5	29.4	374	4	Q82663	Q82663 homo sapien
15	371	29.4	375	4	Q82495	Q82495 homo sapien
16	369	29.2	330	11	Q8R142	Q8r142 mus.musculu



```
DR GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW RECEPTOR.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AB3D345C6 CRC64;

Query Match 31.5%; Score 398.5; DB 4; Length 280;
Best Local Similarity 36.7%; Pred. No. 5.1e-28;
Matches 79; Conservative 48; Mismatches 79; Indels 9; Gaps 3;

QY 4 KPKVSLNPPMNRIFKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIIVNAKFEES 63
DB 21 KAVITLQPPVSVFQETVTLHCEVLHLPSSSTQFLNGTATQTSFYRITSASVND 80
QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVVKVIYKD 123
DB 81 GEYRCQGLSGRSDPTQLSEIHRGWLQLQVSSRVFMEGEPLALRCHAWKDKLVNLYYRN 140
QY 124 GEALKYWNHNISITNATVDSGTYCTGKWQLDYSEPLNITVIKAPR--EKVWLQF 181
DB 141 GRAKFFHNWNLTKLTNINSHGTGVCSG-MGKHRYTSAGISQYTVKGLQLPTPVWFHV 199
QY 182 FIPLLVILFAVDTLGFIQTQQOVTFLKIKRTRK 216
DB 200 LFVLAVGIMFLVNTVLTWIRKE-----LKRKKK 228

RESULT 5
Q9N216 PRELIMINARY; PRT; 249 AA.
AC Q9N216;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16.
GN Felis silvestris catus (Cat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20180233; PubMed=10713347;
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA Mikami T., Takahashi E.;
RT "Molecular cloning and sequencing of the cDNA encoding the feline
RT Fc(gamma)RIIIA (CD16) homologue.";
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 31.3%; Score 396; DB 6; Length 249;
Best Local Similarity 39.4%; Pred. No. 7.4e-28;
Matches 84; Conservative 33; Mismatches 90; Indels 6; Gaps 1;

QY 4 KPKVSLNPPMNRIFKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIIVNAKFEES 63
DB 25 KAMVLEPEMNRVLVSDGVILKCEGAYPPGDNQAQWHNGSVIPHRAPSYSEIARSEDS 84
QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVVKVIYKD 123
DB 85 GEYKCOGLSASDPVQLVHTGWLLOAPRWVQEGDTQLRCHSKNKTQVKQVYFQD 144
QY 124 GEALKYWNHNISITNATVDSGTYCTGKWQLDYSEPLNITVIKAPR-----Y 177
DB 145 GEYKFFPHKNSDFYIPKATSKHSGSYFCRGLIGNKNSSEAVNITVQGPVPSTSTFLPH 204
QY 178 WLQFFIPLLVILFAVDTLGFIQTQQOVTFLK 210
DB 205 WYQIAFFLVLTALLFVVDTLGHVAVQRLQSSVK 237

RESULT 7
Q9N22 PRELIMINARY; PRT; 256 AA.
AC Q9N22;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16A.a'.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX H. B., Yim D., Kim Y.-S., Swanson T., Kim Y.B.;
RT "Molecular Characterization of Porcine CD16 Isoforms.";
RT
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE FC gamma receptor III.  
GN FCGR3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RT Fossati Jimack L., Boucrot E., Izui S.;  
RA "Mouse Fc gamma R11: identification and characterization of a new  
RT allele in C57BL/6 mice."  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Ovary, and Uterus;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium.  
RN [3]  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AF197930; AG28520.1; -;  
DR EMBL; AK077227; BAC36696.1; -;  
DR MGD; MGI:95500; Fcgr3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Receptor.  
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;  
  
Query Match 30.4%; Score 384; DB 11; Length 261;  
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DB 34 KAVVLDPPWIVQLKEDMTLMCEGTHNPGNSSTQWFHNSIRSQSSYTF-KATVND 92  
  
QY 63 SGEYKCOHQVNESEPVLEFSDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122  
DB 93 SGEYRCQMEQRLSDPDVLDGIVSDWLLLOQTPQVLEGETITLRCHSWRNKLNIRSFPH 152  
  
QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV-----IKAPRE 178  
DB 153 NEKSVRHHYKNSFIPKANHSBGDYCKSLGSGTQHQSKPTIIVQDPATTSSISLW 212  
  
QY 179 LQFFIPLLVILFAVDTCGLFISTQQV 205  
DB 213 YHTAFSLVMCLLFAVDTCGLFYVRRNL 239  
  
RESULT 11  
QY 08R2R4 PRELIMINARY; PRT; 249 AA.  
AC Q8R2R4;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN FCRL3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027310; AAH27310.1; -;  
DR MGD; MGI:2179523; Fcrl3.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 249 AA; 28372 MW; 740D6BE8E1536224 CRC64;  
  
Query Match 30.3%; Score 382.5; DB 11; Length 249;  
Best Local Similarity 38.9%; Pred. No. 1.2e-26;  
Matches 81; Conservative 38; Mismatches 78; Indels 11; Gaps 2;  
  
QY 3 QPKVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNSGSLSEETNSLIVNAKPED 62  
DB 23 QKAVVLDPPWVRLEEDSVTLRCQGTFSPEDNSIKWFHNSLIPHQDANYVIQSAVKD 82  
  
QY 63 SGEYKCOHQVNESEPVLEFSDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122  
DB 83 SGMVRCQPTALSTISDPVQLEVHMGWLLLTQTKWLFQBGDPIHLRCHSWQNRVPRKVYSQ 142  
  
QY 123 DGEALKWYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITV-----IKAPRE 175  
DB 143 NGKGGKYPHENSELLIPKATENDSGSVFCRGLGHNNKSSASFRISLGDGPGSPMFP-- 200  
  
QY 176 KYWLQFFIPLLVILFAVDTCGLFISTQQ 203  
DB 201 --WQITFCLLIGLLFAIDTVLYFSVRR 226  
  
RESULT 12  
QY 08SPW5 PRELIMINARY; PRT; 357 AA.  
AC Q8SPW5;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE FC gamma receptor I.  
GN FCGR1.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
OC Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Nannuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.B.M.,  
RA Presta L.G.;  
RT "Binding of human IgG to cynomolgus FcR.1";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF485812; AAL92095.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00409; Ig; 3.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
KW Receptor.  
SQ SEQUENCE 357 AA; 40715 MW; F5C51A06A3BCE08F CRC64;  
  
Query Match 29.8%; Score 376.5; DB 6; Length 357;  
Best Local Similarity 41.0%; Pred. No. 6.9e-26;  
Matches 68; Conservative 36; Mismatches 61; Indels 1; Gaps 1;  
  
QY 4 KPQVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNSGSLSEETNSLIVNAKPEDS 63  
DB 21 KAVITLQPPWVSFQETVTLQCEVPRLPFGSSSTQWFLNGTATQTSTPSYRITSASVKDS 80  
  
QY 64 SGEYKCOHQVNESEPVLEFSDWLLLOASAEVVMGQPLFLRCHGWRNWDVYKVIYK 123  
DB 81 GEYRCQSGRSDFIQLEIHRDNLQVSRVFTGEFGLRCHAWKDLVYVLYQN 140

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QY 124 GEALKYWNENHISITNATVDSGYCTGKQWQDYSEPLNITV 169
DB 141 GKAFKFFYNSLTILKTNHNGAYHCSG-MGKHRYTSAGSVTV 185

RESULT 13
Q7TW9
ID Q7TW9 PRELIMINARY; PRT; 261 AA.
AC Q7TW9;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Similar to Fc gamma receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.I., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerk A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052819; AAH52819.1; -.
KW Receptor.
SQ SEQUENCE 261 AA; 30032 MW; 81389D45C2E14730 CRC64;

Query Match 29.4%; Score 372; DB 11; Length 261;
Best Local Similarity 37.7%; Pred. No. 1.2e-25;
Matches 78; Conservative 38; Mismatches 85; Indels 6; Gaps 3;

QY 4 KPKVSLNPPNRIKFGENVTLTCNGNNFFVSVSTKWFHN-GSLSEBTNSLNIVNAKFD 62
DB 34 KAVVLPDPPIQVLDKNDVILMEGTHNPNCSNQFWHNSIRSQVSSYTP-KATVND 92

QY 63 SGXEYKCHQVNESEPVYLEVFDWLLQLQASAEVVMGQPLFIRCHGRNNDVYKVIYK 122
DB 93 SGYRCQMEQTRLSDPVDLGVISDWLLLPQVFLFEGEITLRCPSWRNKLNRISPFH 152

QY 123 DGEALKYWNENHISITNATVDSGYCTGKQWQDYSEPLNITV----IKAPKRYW 178
DB 153 NEKSVRYHHYKSNFSPKFNHSHSGDYKSGLSGTQHOSKPVITTVQDPATTSSISLW 212

QY 179 LQFFIPLLVILFAVDTFGLFISTQQOV 205
DB 213 HHTAFSLVMLCLLFAVDIGLYFYVRNL 239

RESULT 14

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AC Q92663;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fc gamma receptor 1.
GN Al.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Forges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
cells.";
RL J. Clin. Invest. 90:2102-2109 (1992).
DR EMBL; L03418; AAA36049.1; -.
DR FIR; A39878; A39878.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 374 AA; 42632 MW; D33D59398CEBA699 CRC64;

Query Match 29.4%; Score 371.5; DB 4; Length 374;
Best Local Similarity 41.0%; Pred. No. 2.1e-25;
Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

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DB 21 KAVITLQPPWVSVFQETVTLHCEVLPUGSSSTQWFLNGTATQTPTSPYRITSASVND 80

QY 64 GEYKCHQVNESEPVYLEVFDWLLQLQASAEVVMGQPLFIRCHGRNNDVYKVIYK 123
DB 81 GEYRCQGLSGRSDPIQLIHRGWLLQVSRVTEGEPLALRCHAKDKLVNVLVYRN 140

QY 124 GEALKYWNENHISITNATVDSGYCTGKQWQDYSEPLNITV 169
DB 141 GKAFKFFHNSLTILKTNHNGYHCSG-MGKHRYTSAGISVTV 185

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AC Q92495;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fc gamma receptor type 1 (Fc gamma RIB=Fc gamma receptor).
GN CD64 OR FC-GAMMA-RIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Ravesh D.,
RA Ezekowitz A.B.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-224 FROM N.A.
RX MEDLINE=93018627; PubMed=1402657;
RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Ravesh D.P.,
RA Ezekowitz R.A.;

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6	699	100.0	1068	6	AX026808	AX026808 Sequence
7	699	100.0	1081	9	HOMMCIAA	U03605 Human mast
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14	699	100.0	1198	6	AX101304	AX101304 Sequence
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19	696	99.6	696	6	AX074290	AX074290 Sequence
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ALIGNMENTS

RESULT 1  
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LOCUS Sequence 7 from patent US 6309832.  
DEFINITION ARI75483  
ACCESSION ARI75483  
VERSION ARI75483.1 GI:17916782  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 699)  
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wasson,D.L.  
TITLE Method to detect IGE  
JOURNAL Patent: US 6309832-A 7 30-OCT-2001;  
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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ORIGIN	ORIGIN		
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Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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DB	1 GTCCCTCAGAACCTTAAGTCTCCTTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60	DB	76 GTCCCTCAGAACCTTAAGTCTCCTTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 135
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DB	61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120	DB	136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCAATGGTTC 195
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DB	181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240	DB	256 GAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315
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DEFINITION	Sequence 4 from patent US 6309832.	DEFINITION	Sequence 5 from patent US 6309832.
ACCESSION	AR175481	ACCESSION	AR175482
VERSION	AR175481.1	VERSION	AR175482.1
KEYWORDS	GI:17916780	KEYWORDS	GI:17916781
SOURCE	Unknown.	SOURCE	Unknown.
ORGANISM	Unknown.	ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 774)	REFERENCE	1 (bases 1 to 774)
AUTHORS	Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.	AUTHORS	Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE	Method to detect IGE	TITLE	Method to detect IGE
JOURNAL	Patent: US 6309832-A 4 30-OCT-2001;	JOURNAL	Patent: US 6309832-A 5 30-OCT-2001;
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Best Local Similarity	100.0%;	Pred. No. 7.5e-199;		
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61	AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC	120	QY
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121	CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT	180	QY
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181	GAGACAGATGGAGAATACAAATGTGAGCACCAACAAGTTAATGAGAGTGAACTGTGTAC	240	QY
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301	CAGCCCTCTTCTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTAT	360	QY
415	CAGCCCTCTTCTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTAT	474	DB
361	TATAAGGATGGTGAAGCTCTCAAGTACTGTGTTATGAGAACCAACATCTCCATTACAAT	420	QY
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579	Db	CACAATGGCAGCCCTTTCAGAAGAGACAAAATTCAGTTTGAATATTGTGAATGCCAAATTT	520
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519	Db	GAAGACAGTGGAGNAACAATCTCAGCACCAACAGTTAATGACAGTGRAACCTGTGTAC	460
241	QY	CTGAAGTCTTTCAGTGACTGGCTGCTCTTCAGGCCCTCTGTCAGGTGGTGATGAGGGC	300
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VERSION	A21606.1	GI:579605		
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SOURCE	.	Homo sapiens		
ORGANISM	.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. . (bases 1 to 1068)		
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AUTHORS	.			
TITLE	HYBRID FC RECEPTOR MOLECULES			
JOURNAL	Patent: WO 9108570-A 29 16-MAY-1991;			

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DEFINITION
Recombinant soluble Fc receptors.
ACCESSION
BD264325
VERSION
BD264325.1 GI:33074093
KEYWORDS
JP 2002531086-A/8.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sondermann, P., Huber, R. and Jakob, U.
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Patent: JP 2002531086-A 8 24-SEP-2002;
MAX PLANCK GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV
COMMENT
OS Homo sapiens (human)
PN JP 2002531086-A/8
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585398
PI PETER SONDERMANN, ROBERT HUBER, UWE JAKOB
PC C12N15/09, A61K38/00, A61K45/00, A61P19/02, A61P29/00, A61P31/18,
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Best Local Similarity 100.0%; Pred. No. 7.5e-199;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Sequence 14 from Patent EP1006183.
ACCESSION
AX026808
VERSION
AX026808.1 GI:10187941
KEYWORDS
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SOURCE
Homo sapiens
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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AUTHORS
Recombinant soluble fc receptors
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JOURNAL
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 ACCESSION J03605.1 GI:187449  
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 SOURCE  
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Shimizu, A., Tepler, I., Benfey, P.N., Berenstein, E.H., Siraganian, R.P. and Leder, P.  
 TITLE Human and rat mast cell high-affinity immunoglobulin E receptors: characterization of putative alpha-chain gene products  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (6), 1907-1911 (1988)  
 MEDLINE 88158102  
 PUBMED 2964540  
 COMMENT Original source text: Human mast cell line KU812, cDNA to mRNA, clone pAS-h-IgPR-110B.  
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BC005912 1102 bp mRNA linear PRI 03-OCT-2003  
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 complete cds.  
 BC005912  
 BC005912.1 GI:13543505  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Carninci, P., Brownstein, M.J., Usdin, T.B., Ioshiki, S.,  
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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MEDLINE  
PUBMED  
12477932  
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Direct Submission  
Strausberg, R.  
Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC) Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONTECH  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcdpaxil.stanford.edu](mailto:mcdpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILML at: <http://image.llnl.gov>  
Series: IRAL Plate: 21 Row: h Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503674.

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DEFINITION Sequence 10 from patent US 6171803.  
ACCESSION AR123794  
VERSION AR123794.1 GI:14109155  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1174)  
AUTHORS Kinet, J.Pierre.  
TITLE Isolation, characterization, and use of the human .beta. subunit of the high affinity receptor for immunoglobulin E  
JOURNAL Patent: US 6171803-A 10 09-JAN-2001;  
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 ACCESSION AX074287  
 VERSION AX074287.1 GI:12710474  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Weber, E.R., Wood, K.V. and Hall, M.P.  
 TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof  
 JOURNAL Patent: WO 0104310-A 1 18-JAN-2001;  
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 ACCESSION AX074289  
 VERSION AX074289.1 GI:12710476  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1  
AUTHORS Weber, E.R., Wood, K.V. and Hall, M.P.  
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof  
JOURNAL Patent: WO 0104310-A 3 18-JAN-2001;  
Heska Corporation (US); PROMEGA CORPORATION (US)  
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LOCUS AX101304 1198 bp DNA linear PAT 10-APR-2001  
DEFINITION Sequence 7 from Patent WO0121816.  
ACCESSION AX101304  
VERSION AX101304.1 GI:13620094

KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Kinet, J.P., Donnadieu, E., Jouvin, M.H., Cookson, W. and Woffatt, M.F.  
TITLE Modulation of Ige receptor cell surface expression  
JOURNAL Patent: WO 0121816-A 7 29-MAR-2001;  
ISIS INNOVATION LIMITED (GB); Beth Israel Deaconess Medical Center, Inc. (US)  
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DEFINITION Sequence 6130 from Patent WO0194629.  
ACCESSION AX335621  
VERSION AX335621.1 GI:18126340  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrihan, S., Soppet, D.R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 6130 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	699	100.0	1198	2 Aav36343	Aav36343 cDNA enco
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12	699	100.0	1198	6 Aab67793	Aab67793 Oesophagu
13	699	100.0	1198	7 Aab296629	Aab296629 Human hig
14	699	100.0	1198	9 Aab85535	Aab85535 Human imm
15	699	100.0	21742	3 Aaa34816	Aaa34816 Human ade
16	699	100.0	21742	7 Aaf20938	Aaf20938 Human hig
17	699	100.0	21742	7 Aab296632	Aab296632 Human hig
18	699	100.0	117608	7 Aab297129	Aab297129 Human rec
19	699	100.0	117609	3 Aaf21435	Aaf21435 Human rec
20	698	99.9	773	6 Aab52959	Aab52959 Human cdn
21	697.4	99.8	898	8 Acd06182	Acd06182 Human cdn
22	696.4	99.6	773	2 Aav20402	Aav20402 Human IGE
23	696	99.6	696	5 Aaf24914	Aaf24914 Complemen

24	696	99.6	696	5 AAF24913	Aaf24913 Nucleotid
25	695.8	99.5	1193	2 AAQ04644	AaQ04644 Encodes a
26	695.8	99.5	1199	2 AAQ14736	AaQ14736 Human Fc(
27	547	78.3	570	3 AAA27472	Aaa27472 Recombina
28	540.8	77.4	1150	2 AAQ34840	AaQ34840 Human hig
29	537.8	76.9	2955	2 AAV20404	Aav20404 Plasmid R
30	537.8	76.9	2955	6 ABS52957	AbS52957 Human CDN
31	534	76.4	851	2 AAQ27267	AaQ27267 Human FCE
32	528	75.5	528	3 AAA27301	Aaa27301 Human Fce
33	528	75.5	528	4 AAH47768	Aah47768 Nucleotid
34	516	73.8	516	3 AAA27302	Aaa27302 Human nhf
35	516	73.8	516	5 AAF24917	Aaf24917 Complemen
36	516	73.8	516	5 AAF24918	Aaf24918 Complemen
37	516	73.8	591	5 AAF24915	Aaf24915 DNA enco
38	516	73.8	591	5 AAF24916	Aaf24916 Complemen
39	516	73.8	713	2 AAQ55969	AaQ55969 Human dih
40	516	73.8	1908	5 AAF24923	Aaf24923 Fc epsilo
41	516	73.8	1908	5 AAF24928	Aaf24928 Fc epsilo
42	516	73.8	1983	5 AAF24927	Aaf24927 Fc epsilo
43	516	73.8	1983	5 AAF24926	Aaf24926 Fc epsilo
44	516	73.8	2193	5 AAF24923	Aaf24923 Complemen
45	516	73.8	2268	5 AAF24921	Aaf24921 Complemen

ALIGNMENTS

RESULT 1  
AAF97964  
ID AAF97964 standard; cDNA; 774 BP.

AC AAF97964;  
XX  
DT 19-JUN-2001 (first entry)

DE Human immunoglobulin E receptor I alpha subunit coding sequence.

XX Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;  
KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;  
KW immunoassay; detection; ss.

OS Homo sapiens.

XX WO20011010-A2.

XX 15-FEB-2001.

XX 02-AUG-2000; 2000WO-US021097.

XX 09-AUG-1999; 99US-0147860P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;

XX Stephens JC;

XX WPI; 2001-202766/20.

XX P-PSDB; AAB74667.

XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms

XX in the immunoglobulin E receptor I alpha subunit gene.

XX Claim 7; Fig 2; 99pp; English.

XX The present invention describes an isolated polynucleotide (I) comprising  
a nucleotide sequence (S) which is a polymorphic variant of a reference  
sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)  
gene or its fragment. The polymorphic variant comprises at least one  
polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,  
PS10 or PS11, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine  
(A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at  
PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide  
251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at

CC a position corresponding to nucleotide 530. (I) can be used in gene  
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)  
 CC encoded by (I) is useful in drug screening assays and in assays to  
 CC measure the binding affinity of one or more candidate drugs targeting  
 CC (II). An antibody (III) is useful to immunoprecipitate (II) from  
 CC solution and also reacts with (II) on Western or immunoblots of  
 CC polyacrylamide gels on membrane supports or substrates. (III) is also  
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to  
 CC AAF98096 represent IGRA allele specific oligonucleotide probes; AAF98097  
 CC to AAF98140 represent IGRA gene polymorphism detection primers; and  
 CC AAF98141 to AAF98180 represent IGRA gene PCR primers which are used in  
 CC the exemplification of the present invention. The present sequence  
 CC encodes the human IGRA protein used in the present invention  
 XX  
 SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 4; Length 774;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGTCTCTGAACTCCATGGAATAGATATTTAAAGGAGAG 60  
 DB 76 GTCCTCAGAACCTTAAGTCTCTGAACTCCATGGAATAGATATTTAAAGGAGAG 135  
 QY 61 AATGTGACTCTTAATGTAATGGGAAACAATTTCTTGAAGTCTCCACCAATGGTTC 120  
 DB 136 AATGTGACTCTTAATGTAATGGGAAACAATTTCTTGAAGTCTCCACCAATGGTTC 195  
 QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGATGTCACCAATTT 180  
 DB 196 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGATGTCACCAATTT 255  
 QY 181 GAACAGAGTGGAGAAATCAAAATGTGACACCAACAAATTAATGAGAGTGAACCTGTGAC 240  
 DB 256 GAACAGAGTGGAGAAATCAAAATGTGACACCAACAAATTAATGAGAGTGAACCTGTGAC 315  
 QY 241 CTGGAAGTCTTCAGTACGCTGCTCTTCAGGCTCTCTGAGGTGGATGGAGGC 300  
 DB 316 CTGGAAGTCTTCAGTACGCTGCTCTTCAGGCTCTCTGAGGTGGATGGAGGC 375  
 QY 301 CAGGCTCTCTTCAGTACGCTGCTCTTCAGGCTCTCTGAGGTGGATGGAGGC 360  
 DB 376 CAGGCTCTCTTCAGTACGCTGCTCTTCAGGCTCTCTGAGGTGGATGGAGGC 435  
 QY 361 TATAGAGTGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 420  
 DB 436 TATAGAGTGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 495  
 QY 421 GCCACAGTGAAGACAGTGAACCTCTACTGTACGGGAAAGTGGAGCTGGACTAT 480  
 DB 496 GCCACAGTGAAGACAGTGAACCTCTACTGTACGGGAAAGTGGAGCTGGACTAT 555  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 540  
 DB 556 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 615  
 QY 541 TTTTATCCCATGTTGGTGGTGTCTGTTGCTGTGGACACAGATTAATTTATCTCA 600  
 DB 616 TTTTATCCCATGTTGGTGGTGTCTGTTGCTGTGGACACAGATTAATTTATCTCA 675  
 QY 601 ACTCAGCAGCAGGTTCACATTTCTTTGAAGATTAAGAGAACCAAGGAAAGGCTTCAGACTT 660  
 DB 676 ACTCAGCAGCAGGTTCACATTTCTTTGAAGATTAAGAGAACCAAGGAAAGGCTTCAGACTT 735  
 QY 661 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACAACTGA 699  
 DB 736 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 2  
 AAA27470  
 ID AAA27470 standard; cdna; 1068 BP.  
 XX

AC AAA27470;  
 XX 11-SEP-2000 (first entry)  
 DT Human Fc receptor, FcpsilonRia, coding sequence.  
 XX  
 DE Human Fc receptor, FcpsilonRia, coding sequence.  
 DE  
 KW Human; Fc receptor; FcpsilonRia; immunoglobulin; infection;  
 KW immune response; HIV; IgG; immunosuppressive; antirheumatic;  
 KW antinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;  
 KW systemic lupus erythematosus; tumour; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FT 31..813  
 FT /\*tag= a  
 FT /product= "FcpsilonRia"  
 XX  
 PN EP1006183-A1.  
 XX 07-JUN-2000.  
 PD 03-DEC-1998; 98EP-00122969.  
 PF 03-DEC-1998; 98EP-00122969.  
 PR 03-DEC-1998; 98EP-00122969.  
 XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 PA  
 XX WPI: 2000-367968/32.  
 DR P-PSDB; AAF96230.  
 XX  
 PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and  
 PT glycosylation, useful for diagnosing and treating immune disorders and  
 PT cancer.  
 PS Disclosure; Page 17; 60pp; English.  
 XX  
 CC The present sequence is the human Fc receptor, FcpsilonRia, coding  
 CC sequence. Fc receptors play a key role in defending the body against  
 CC infections. First, pathogens are opsonised by serum immunoglobulins. The  
 CC resulting complex then binds to cells expressing Fc receptors. Upon Fc  
 CC receptor activation, immune effector pathways are activated, leading to  
 CC immune response. The present sequence may be modified to produce  
 CC recombinant versions. The recombinant Fc receptor consists only of the  
 CC extracellular portion of the receptor and are not glycosylated i.e. they  
 CC do not have transmembrane domains or signal peptides. The recombinant  
 CC proteins may be used in immunoassays to determine the immune status of  
 CC patients with chronic diseases of the immune system, e.g. AIDS, systemic  
 CC lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid  
 CC arthritis. In addition, pharmaceutical compositions containing  
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,  
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM  
 XX  
 SQ Sequence 1068 BP; 330 A; 215 C; 229 G; 294 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 3; Length 1068;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGTCTCTGAACTCCATGGAATAGATATTTAAAGGAGAG 60  
 DB 115 GTCCTCAGAACCTTAAGTCTCTGAACTCCATGGAATAGATATTTAAAGGAGAG 174  
 QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTGAAGTCTCCACCAATGGTTC 120  
 DB 175 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTGAAGTCTCCACCAATGGTTC 234  
 QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGATGTCACCAATTT 180  
 DB 235 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGATGTCACCAATTT 294  
 QY 181 GAACAGAGTGGAGAAATCAAAATGTGACACCAACAAATTAATGAGAGTGAACCTGTGAC 240

Db 295 GAAGACAGTGGAGATACAAATGTGACGACCAACCAAGTTAATGAGTGAACCTGTGTAC 354  
 QY 241 CTGGAAGTCTTCAGTCACTGGTGTCTCTTCAGGCTCTGCTGAGTGTGTGAGGAGGC 300  
 Db 355 CTGGAAGTCTTCAGTCACTGGTGTCTCTTCAGGCTCTGCTGAGTGTGTGAGGAGGC 414  
 QY 301 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACTGGATGTGTACAGGTGATCTAT 360  
 Db 415 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACTGGATGTGTACAGGTGATCTAT 474  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAATCTCCATTACAAAT 420  
 Db 475 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAATCTCCATTACAAAT 534  
 QY 421 GCCACAGTTCAAGACAGTGGAACTTACTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 480  
 Db 535 GCCACAGTTCAAGACAGTGGAACTTACTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 594  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTTACAA 540  
 Db 595 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTTACAA 654  
 QY 541 TTTTATATCCATTGTTGGTGTGATCTGTTTGTGTGTGACACAGGATTTATCTCA 600  
 Db 655 TTTTATATCCATTGTTGGTGTGATCTGTTTGTGTGTGACACAGGATTTATCTCA 714  
 QY 601 ACTCAGCAGCAGTCACTTCTCTCAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 660  
 Db 715 ACTCAGCAGCAGTCACTTCTCTCAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 774  
 QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
 Db 775 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 813

RESULT 3

ID AAN90126  
 AC AAN90126;  
 XX  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 01-NOV-1989 (first entry)  
 XX  
 DE cDNA encoding human mast cell IgE receptor alpha subunit.  
 XX  
 XX cDNA; immunoglobulin E receptor alpha subunit; treats allergies;  
 KW design non-peptide drugs; human.  
 XX  
 OS Homo sapiens; (Human); mast cell line.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 35..805  
 FT /\*tag= a  
 FT  
 FN W08905352-A.  
 FN  
 PD 15-JUN-1989.  
 XX  
 XX 29-NOV-1988; 88WO-US004255.  
 XX  
 XX 01-DEC-1987; 87US-00127214.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 PA (USSH ) NAT INST OF HEALTH.  
 PA  
 XX Leder P, Benfey P;  
 XX  
 XX WPI; 1989-192698/26.  
 DR P-PSDB; AAP90385.  
 XX

PT CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.  
 XX Disclosure; Fig 4; 17pp; English.  
 XX  
 CC cDNA sequence encoding immunoglobulin E receptor alpha subunit of human  
 CC mast cell IGE surface receptor (see corresp. AAP90385). Used to produce  
 CC antibodies which can diagnose IGE receptor levels, measure and treat  
 CC allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to  
 CC correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)  
 XX  
 XX Sequence 1088 BP; 347 A; 216 C; 229 G; 296 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 699; DB 1; Length 1088;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCCTCAGAACCTTACAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 60  
 Db 110 GTCCCTCAGAACCTTACAGTCTCTTGAACCTCCATGGAATAGAAATTTAAAGGAGAG 169  
 QY 61 AATGTGACTCTTACATGTAAATGGGAACAAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 120  
 Db 170 AATGTGACTCTTACATGTAAATGGGAACAAATTTCTTTGAAAGTCAGTTCCACCAATGGTTC 229  
 QY 121 CACAATGGCAGCCTTTTCAGAAAGACAAATTCAGTTTGAATATATGTAATGCCAAATTT 180  
 Db 230 CACAATGGCAGCCTTTTCAGAAAGACAAATTCAGTTTGAATATATGTAATGCCAAATTT 289  
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 290 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 349  
 QY 241 CTGGAAGTCTTCAGTCACTGGCTGCTCTTCAGGCTCTGCTGAGGTTGATGAGAGGC 300  
 Db 350 CTGGAAGTCTTCAGTCACTGGCTGCTCTTCAGGCTCTGCTGAGGTTGATGAGAGGC 409  
 QY 301 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360  
 Db 410 CAGCCCTCTTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 469  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAATCTCCATTACAAAT 420  
 Db 470 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACCAATCTCCATTACAAAT 529  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 480  
 Db 530 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGGTGTGGCAGCTGGACTAT 589  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 540  
 Db 590 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 649  
 QY 541 TTTTATATCCATTGTTGGTGTGATCTGTTTGTGTGTGGACACAGGATTTATCTCA 600  
 Db 650 TTTTATATCCATTGTTGGTGTGATCTGTTTGTGTGTGGACACAGGATTTATCTCA 709  
 QY 601 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 660  
 Db 710 ACTCAGCAGCAGTCACTTCTCTTGAAGATTAGAGAACCAAGAAAGCTTTCAGACTT 769  
 QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
 Db 770 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 808

RESULT 4  
 AAO51020  
 ID AAO51020 standard; DNA; 1174 BP.  
 XX  
 XX AAO51020;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 21-JUN-1994 (first entry)  
 DT



XX DE Human FcεRI alpha gene.  
 XX KW IgE; immunoglobulin E receptor; beta subunit; basophils; allergy;  
 XX KW aggregation; signal transduction; diagnosis; antagonist; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 107..881  
 XX FT /\*tag= a  
 XX  
 XX PN WO9321317-A1.  
 XX PD 28-OCT-1993.  
 XX PF 16-APR-1993; 93WO-US003419.  
 XX PR 16-APR-1992; 92US-00869933.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX PI Kinet JP;  
 XX DR WPI; 1993-351727/44.  
 XX DR P-PSDB; AAR42336.  
 XX  
 XX PT Immunoglobulin E receptor human beta sub-unit isolation - using 1st  
 XX PT strand reverse transcripts from human basophils as templates for a  
 XX PT polymerase chain reaction, used to treat and diagnose allergic diseases.  
 XX PS Claim 1; Fig 1; 154pp; English.  
 XX  
 XX The sequence is that of the human FcεRI alpha subunit, isolated by using  
 XX first strand reverse transcriptase from human basophils by PCR. The gene  
 XX and its prod. can be used to identify human beta subunit FcεRI inhibitors  
 XX (immunoglobulin E receptor) which inhibit the binding of IgE to its  
 XX receptor and inhibit the aggregation function of the receptor or the  
 XX signal transducing function related to allergic response. Such inhibitors  
 XX can be used for the treatment or prevention of allergic disease. See also  
 XX AA051021-4. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 1174 BP; 378 A; 240 C; 241 G; 315 T; 0 U; 0 Other;  
 XX  
 XX Query Match 100.0%; Score 699; DB 2; Length 1174;  
 XX Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
 XX Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 GTCCTCAGAACTCAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60  
 XX DB 182 GTCCTCAGAACTCAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 241  
 XX QY 61 AATGTGACTCTTACATGTAATGGAAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120  
 XX DB 242 AATGTGACTCTTACATGTAATGGAAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 301  
 XX QY 121 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATGTAATGCAATTT 180  
 XX DB 302 CACATGCGACCTTTTCAGAGAGACAAATTCAGTTTGAATATGTAATGCAATTT 361  
 XX QY 181 GAAGACAGTGGAGAAATCAAAATGTGACACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
 XX DB 362 GAAGACAGTGGAGAAATCAAAATGTGACACCAAGTTAATGAGAGTGAACCTGTGTAC 421  
 XX QY 241 CTGGAAGTCTTCAGTGAAGTGGTCTCTTCAGGCTCTCTGAGGTGGTGAAGGGC 300  
 XX DB 422 CTGGAAGTCTTCAGTGAAGTGGTCTCTTCAGGCTCTCTGAGGTGGTGAAGGGC 481  
 XX QY 301 CAGCCCTCTTCTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTAT 360  
 XX DB 482 CAGCCCTCTTCTCTCAGTGGCCATGGTTGGAGGAACCTGGGATGTGTACAGGTGATCTAT 541  
 XX QY 361 TATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

DB 542 TATAGAGTGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 601  
 QY 421 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGACTAT 480  
 DB 602 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGACTAT 661  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAGTACTGGCTACAA 540  
 DB 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAGTACTGGCTACAA 721  
 QY 541 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTGTGGACACAGGATTTATCTCA 600  
 DB 722 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTGTGGACACAGGATTTATCTCA 781  
 QY 601 ACTCAGCAGCAGTGCACATTTCTCTGAAGATTAGAGAACCGAGAAAGCTTCAGACTT 660  
 DB 782 ACTCAGCAGCAGTGCACATTTCTCTGAAGATTAGAGAACCGAGAAAGCTTCAGACTT 841  
 QY 661 CTGAACCCACATCTCTTAAGCCAAACCCCAAACTGA 699  
 DB 842 CTGAACCCACATCTCTTAAGCCAAACCCCAAACTGA 880  
 XX  
 XX RESULT 5  
 XX AAT85615  
 XX ID AAT85615 standard; cDNA; 1197 BP.  
 XX AC AAT85615;  
 XX DT 04-FEB-1998 (first entry)  
 XX  
 XX Alpha subunit of human high affinity receptor for IgE (human FcεRI) cDNA.  
 XX KW alpha subunit; human high affinity receptor; IgE; FcεRI; antigen;  
 XX KW preformed mediator; histamine; serotonin; leukotriene; IgE level;  
 XX KW allergic condition; therapy; allergic response; drug screening;  
 XX KW DNA probe; diagnostic assay; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT CDS 106..880  
 XX FT /\*tag= a  
 XX FT /product= "human\_FcεRI\_alpha\_subunit"  
 XX FT sig\_peptide 106..181  
 XX FT /\*tag= b  
 XX FT mat\_peptide 182..877  
 XX FT /\*tag= c  
 XX FT /product= "alpha\_subunit"  
 XX  
 XX PN US5639660-A.  
 XX XX 17-JUN-1997.  
 XX XX 24-FEB-1988; 88US-00160457.  
 XX XX 24-FEB-1988; 88US-00160457.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PA (HOFF ) HOFFMANN LA ROCHE INC.  
 XX PI Kochan JP, Kinet JP;  
 XX DR WPI; 1997-332052/30.  
 XX DR P-PSDB; AAW24066.  
 XX  
 XX DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin  
 XX E - used for producing polypeptide(s) which can be used for therapy or to  
 XX prevent allergic responses or in diagnostic and screening assays.  
 XX Claim 1; Fig 1A-B; 15pp; English.



CC This cDNA sequence encodes the alpha subunit of the human high affinity  
CC receptor for IgE (FcERI). FcERI is found exclusively on mast cells,  
CC basophils and related cells. Aggregation of IgE occupied FcERI by antigen  
CC triggers both the release of of preformed mediators such as histamine and  
CC serotonin, as well as stimulating the synthesis of leukotrienes. It is  
CC the release of these mediators that results in an allergic condition. The  
CC DNA can be used to produce the human FcERI alpha polypeptides which can  
CC be used for therapy or to prevent allergic responses, in drug screening  
CC assays or for monitoring IgE levels in patients. The DNA can also be used  
CC to produce DNA probes useful in diagnostic assays  
XX  
XX  
SQ Sequence 1197 BP; 389 A; 242 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 2; Length 1197;  
Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 60  
Db 181 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 240  
QY 61 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120  
Db 241 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 300  
QY 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATTTGAATGTCAGTTCACCAAAATTT 180  
Db 301 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATTTGAATGTCAGTTCACCAAAATTT 360  
QY 181 GAGACAGTGGAGATCAAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 361 GAGACAGTGGAGATCAAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 420  
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGCCTCTCTGAGGTGGTGTAGAGGGC 300  
Db 421 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGCCTCTCTGAGGTGGTGTAGAGGGC 480  
QY 301 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGACCTGGATGTACAGAGTGAATCTAT 360  
Db 481 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGACCTGGATGTACAGAGTGAATCTAT 540  
QY 361 TATAAGCATGCTGAAGTCTCAAGTACTGGTATGAGACCAACCAATCTCCATTACAAAT 420  
Db 541 TATAAGCATGCTGAAGTCTCAAGTACTGGTATGAGACCAACCAATCTCCATTACAAAT 600  
QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTCAGGGGCAAGTGTGGCAGCTGGACTAT 480  
Db 601 GCCACAGTTGAAGCAGTGGAACTTACTGTCAGGGGCAAGTGTGGCAGCTGGACTAT 660  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATATAAGCTCCGCTGAGAAGTACTGGCTACAA 540  
Db 661 GAGTCTGAGCCCTCAACATTTACTGTATATAAGCTCCGCTGAGAAGTACTGGCTACAA 720  
QY 541 TTTTATPCCCATTTGTTGGTGGTGAATCTGTTTCTGTGGACACAGGATTTATCTCA 600  
Db 721 TTTTATPCCCATTTGTTGGTGGTGAATCTGTTTCTGTGGACACAGGATTTATCTCA 780  
QY 601 ACTGAGCAGAGGTGACATTTCTTCTGAGATTAAGAGACCAAGGAGGCTTCAGACTT 660  
Db 781 ACTGAGCAGAGGTGACATTTCTTCTGAGATTAAGAGACCAAGGAGGCTTCAGACTT 840  
QY 661 CTGAACCCACATCTCTTAAGCCAAAACCCCAAAACCACTGA 699  
Db 841 CTGAACCCACATCTCTTAAGCCAAAACCCCAAAACCACTGA 879

RESULT 6  
ID AAV36343  
XX AAV36343 standard; cDNA; 1198 BP.  
AC AAV36343;  
XX AAV36343;  
DT 07-OCT-1998 (first entry)

XX cDNA encoding the alpha chain of a Fc epsilon receptor.  
DE  
XX Alpha chain; human; Fc epsilon receptor; canine; equine; feline;  
KW immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;  
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;  
KW flea allergy; heartworm infection; ds.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT 107..880  
FT CDS /\*tag= a  
XX WO9823964-A1.  
XX 04-JUN-1998.  
XX 24-NOV-1997; 97WO-US021651.  
XX 26-NOV-1996; 96US-00756387.  
XX (HESK-) HESKA CORP.  
XX Frank RG, Porter JP, Rushlow KE, Wassom DL;  
XX WPI: 1998-322873/28.  
XX P-PSDB; AAW61190.  
XX Detection of non-human immunoglobulin E - by complex formation with human  
PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic  
PT disease.  
XX Claim 11; Page 36-37; 70pp; English.  
XX The present sequence encodes the alpha chain of the human Fc epsilon  
CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)  
CC comprises reacting isolated human Fc epsilon receptor with the test  
CC sample and detecting formation of a IgE-receptor complex. Detection of  
CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,  
CC internal parasitic infections or B cell neoplasia, and for measuring  
CC effect of treatments. Most particularly flea allergy in dogs and cats is  
CC detected, and also heartworm infection  
XX  
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 699; DB 2; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 60  
Db 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 241  
QY 61 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120  
Db 242 AATGTGACTCTTACATGATGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 301  
QY 121 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATTTGAATGTCAGTTCACCAAAATTT 180  
Db 302 CACAATGGCAGCCTTTGAGAGAGACAAATTCAGTTTGAATTTGAATGTCAGTTCACCAAAATTT 361  
QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAAGACAGTGGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 421  
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGCCTCTCTGAGGTGGTGTAGTGGAGGGC 300  
Db 422 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGCCTCTCTGAGGTGGTGTAGTGGAGGGC 481  
QY 301 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACTGGATGTGTACAGGTGTATCTAT 360  
Db 482 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACTGGATGTGTACAGGTGTATCTAT 541

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACCAATCTCCATTACAAAT 420  
 Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACCAATCTCCATTACAAAT 601  
 QY 421 GCCACAGTTGAGACAGTGGACCTACTACTGTAGGGGCAAGTGTGCGAGCTGACTAT 480  
 Db 602 GCCACAGTTGAGACAGTGGACCTACTACTGTAGGGGCAAGTGTGCGAGCTGACTAT 661  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTCAA 540  
 Db 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTCAA 721  
 QY 541 TTTTATATCCCATTTGTTGGTGTGATTCGTTTGTGTGGACACAGGATTTATCTCA 600  
 Db 722 TTTTATATCCCATTTGTTGGTGTGATTCGTTTGTGTGGACACAGGATTTATCTCA 781  
 QY 601 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAGAGAACCCAGGAAAGCTTCAGACTT 660  
 Db 782 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAGAGAACCCAGGAAAGCTTCAGACTT 841  
 QY 661 CTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTCA 699  
 Db 842 CTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTCA 880

## RESULT 7

AAA34813

ID AAA34813 standard; DNA; 1198 BP.

XX AC

XX AAA34813;

XX 28-JUL-2000 (first entry)

XX DE Human adenosine receptor related polynucleotide SEQ ID NO:2502.

XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;

XX KW phosphorothioate; impaired respiration; inflammation; allergy;

XX KW allergic disease; bronchoconstriction; inhibitor; anti-inflammatory;

XX KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

XX KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

XX KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

XX KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

XX KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX XX

XX FN WO200009525-A2.

XX PD 24-FEB-2000.

XX XX

XX PF 03-AUG-1999; 99WO-US017712.

XX XX

XX PR 03-AUG-1998; 99US-0095212P.

XX XX

XX PA (UVEC-) UNIV EAST CAROLINA.

XX XX

XX PT Nyce JW;

XX XX

XX DR WPI; 2000-205971/18.

XX XX

XX PT New antisense oligonucleotides useful for treating e.g. pulmonary

XX PT vasoconstriction, inflammation, allergies, asthma, hypertension,

XX PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

XX PT cancers.

XX PT

XX XX

XX PS Disclosure; Page 655; 1343pp; English.

XX XX

XX CC The present invention describes a new composition comprising an antisense

XX CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

XX CC nucleic acids involved in bronchoconstriction, allergies, and/or

XX CC inflammation. The ON can have anti-inflammatory, antiallergic,

XX CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992), are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 CC XX

SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 699; DB 3; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;  
 Matches 699; Conservative 0; Mismatches 0;

QY 1 GTCCCTCAGAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 Db 182 GTCCCTCAGAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 241  
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
 Db 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301  
 QY 121 CACAAATGGCAGGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGCAATGCCAAATTT 180  
 Db 302 CACAAATGGCAGGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGCAATGCCAAATTT 361  
 QY 181 GAAGCAGTGGAGAAATACAAATGTGAGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 362 GAAGCAGTGGAGAAATACAAATGTGAGACCAACCAAGTTAATGAGTGAACCTGTGTAC 421  
 QY 241 CTGGAAGTCTTCAGTGACTGGCTCTCTTCAAGGCTCTGTGAGGCTGGTGTGATGAGGGC 300  
 Db 422 CTGGAAGTCTTCAGTGACTGGCTCTCTTCAAGGCTCTGTGAGGCTGGTGTGATGAGGGC 481  
 QY 301 CAGCCCTCTTCCCTCAGGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
 Db 482 CAGCCCTCTTCCCTCAGGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 541  
 QY 361 TATAGAGTGGTGAAGCTCTCAAGTACTGTATGAGACCAACCAATCTCCATTACAAAT 420  
 Db 542 TATAGAGTGGTGAAGCTCTCAAGTACTGTATGAGACCAACCAATCTCCATTACAAAT 601  
 QY 421 GCCACAGTTGAAGCAGTGGAACTTACTTACTGTAGGGCAAAAGTGTGGCAGCTGACTAT 480  
 Db 602 GCCACAGTTGAAGCAGTGGAACTTACTTACTGTAGGGCAAAAGTGTGGCAGCTGACTAT 661  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 540  
 Db 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGCTGAGAAAGTACTGGCTACAA 721  
 QY 541 TTTTATATCCCATTTGTTGGTGTGATTCGTTTGTGTGGACACAGGATTTATCTCA 600  
 Db 722 TTTTATATCCCATTTGTTGGTGTGATTCGTTTGTGTGGACACAGGATTTATCTCA 781  
 QY 601 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAGAGAACCCAGGAAAGCTTCAGACTT 660  
 Db 782 ACTCAGCAGCGTCAATTTCTCTTGAAGATTAGAGAACCCAGGAAAGCTTCAGACTT 841  
 QY 661 CTGAACCCACATCTCTAAGCCAAACCCCAAAACAACTGA 699

Db 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 880

RESULT 8  
AAF20935  
ID AAF20935 standard; DNA; 1198 BP.  
AC AAF20935;  
XX  
XX  
DT 14-MAR-2001 (first entry)  
DE Human high affinity IgE receptor polynucleotide fragment #2502.  
XX  
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human, airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200062736-A2.  
PN  
XX  
XX 26-OCT-2000.  
PD  
XX  
XX 24-MAR-2000; 2000WO-US008020.  
PF  
XX  
XX 06-APR-1999; 99US-0127958P.  
PR  
XX  
XX (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE/) NYCE J W.  
XX  
XX Nyce JW;  
PI  
XX  
XX WPI; 2000-679539/66.  
DR  
XX  
XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.  
FT  
XX  
XX Disclosure; Page 139; 1592pp; English.  
PS  
XX  
XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,

CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
XX the present invention  
XX  
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
Query Match 100.0%; Score 699; DB 3; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;  
Matches 699; Conservative 0; Mismatches 0;  
XX  
QY 1 GTCCTCAGAAACCTAAGGTCTCTTGAACTCCCTCCATGGAATAGAAATATTAAAGGAGAG 60  
Db 182 GTCCTCAGAAACCTAAGGTCTCTTGAACTCCCTCCATGGAATAGAAATATTAAAGGAGAG 241  
QY 61 AATGAGACTCTTACATGTAATGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGTTTC 120  
Db 242 AATGAGACTCTTACATGTAATGGAACAATTTCTTTGAAAGTCAGTTCCACCAATGTTTC 301  
QY 121 CACATGCGACGCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180  
Db 302 CACATGCGACGCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 361  
QY 181 GAAGACAGTGAGAGATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAAGACAGTGAGAGATACAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421  
QY 241 CTGGAAGTCTTCAGTGACTGCTGCTCTTCAGGCTCTGCTGAGGTGCTGATGAGGCG 300  
Db 422 CTGGAAGTCTTCAGTGACTGCTGCTCTTCAGGCTCTGCTGAGGTGCTGATGAGGCG 481  
QY 301 CAGCCCTCTCTCCTCAGGTGCCATCGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 360  
Db 482 CAGCCCTCTCTCCTCAGGTGCCATCGTTGGAGGAACCTGGGATGTGTACAAGGTGATCTAT 541  
QY 361 TATAAGGATGTTGAAGCTCTCAAGTACTGTAATGAGAACCAACATCTCCATTAACAAT 420  
Db 542 TATAAGGATGTTGAAGCTCTCAAGTACTGTAATGAGAACCAACATCTCCATTAACAAT 601  
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAAAGTGTGCAGCTGGACTAT 480  
Db 602 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAAAGTGTGCAGCTGGACTAT 661  
QY 481 GAGTCTGAGCCCCCTCAACATTACTCTAATAAAAGTCCGCGTGAGAACTGCGGTACAA 540  
Db 662 GAGTCTGAGCCCCCTCAACATTACTCTAATAAAAGTCCGCGTGAGAACTGCGGTACAA 721  
QY 541 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTCGTCACAGGATTTATTTATCTCA 600  
Db 722 TTTTATATCCCATTTGTTGGTGTGATTTCTGTTGTCGTCACAGGATTTATTTATCTCA 781  
QY 601 ACTCAGCAGCAGGTCAACATTTCTTTGAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 660  
Db 782 ACTCAGCAGCAGGTCAACATTTCTTTGAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 841  
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 699  
Db 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACCACTGA 880

RESULT 9  
AAF77692  
ID AAF77692 standard; cDNA; 1198 BP.  
XX  
XX AAF77692;  
AC  
XX  
XX 29-MAY-2001 (first entry)  
DT  
XX Human wild-type FeepsilonRIalpha chain coding sequence.  
DE  
XX Human; FeepsilonRIbeta chain; immunoglobulin E; allergy; atopy;  
KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.  
XX  
XX Homo sapiens.  
OS

XX WO200121816-A1.  
 XX 29-MAR-2001.  
 XX 21-SEP-2000; 2000WO-US025877.  
 XX 21-SEP-1999; 99US-0154924P.  
 XX (ISIS-) ISIS INNOVATION LTD.  
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 XX Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;  
 XX WPI; 2001-266077/27.  
 XX Inhibiting expression of high affinity receptors for immunoglobulin (Ig) E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by contacting cell or administering to subject, a FcεR1β chain variant.  
 XX Disclosure; Page 52; 55pp; English.  
 XX The present invention describes a method of inhibiting the expression of the FcεpsilonR1 receptor by contacting a cell expressing it with an FcεpsilonR1β chain variant. The FcεpsilonR1 receptor is a high affinity receptor for immunoglobulin E. The method is useful in the treatment of allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis, urticaria and angioedema. The present sequence is the wild-type human FcεpsilonR1α chain coding sequence  
 XX SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 699; DB 4; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 DB 182 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 241  
 QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120  
 DB 242 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 301  
 QY 121 CACAATGCCAGCCTTTTCAGAGAGACAAATTCAAAGTTTGAATATGTGAATGCCAAATTT 180  
 DB 302 CACAATGCCAGCCTTTTCAGAGAGACAAATTCAAAGTTTGAATATGTGAATGCCAAATTT 361  
 QY 181 GAAGCAGTGGAGATACAAATGTTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 DB 362 GAAGCAGTGGAGATACAAATGTTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 421  
 QY 241 CTGAAGTCTTTCAGTGAAGTCTCTCTTCAGAGCCTCTGCTGAGGTGGTGTGAGGGG 300  
 DB 422 CTGAAGTCTTTCAGTGAAGTCTCTCTTCAGAGCCTCTGCTGAGGTGGTGTGAGGGG 481  
 QY 301 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAATCGGAATGTGTAAGAGTGAATCTAT 360  
 DB 482 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAATCGGAATGTGTAAGAGTGAATCTAT 541  
 QY 361 TATAAGATGTGAGTCTCACTGACTGTGATGAGAACCAACATCTCCATTACAAAT 420  
 DB 542 TATAAGATGTGAGTCTCACTGACTGTGATGAGAACCAACATCTCCATTACAAAT 601  
 QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTACTCGGGCAAAGTGTGGCAGCTGGACTAT 480  
 DB 602 GCCACAGTTGAAGCAGTGGAACTTACTGTACTCGGGCAAAGTGTGGCAGCTGGACTAT 661  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGGTGTGAGAGTACTGGCTACAA 540  
 DB 662 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCTCCGGTGTGAGAGTACTGGCTACAA 721  
 QY 541 TTTTATATCCATTTGTTGGTGAATCTCTGTTGCTGTGACACAGGATTTATTTATCTCA 600

DB 722 TTTTATATCCATTTGTTGGTGAATTTCTGTTGTCGACACAGGATTTATTTATCTCA 781  
 QY 601 ACTCAGCAGCAGGTTCACATTTCTCTTGAAGATTAAAGAACAGGAAAGCTTCAGACTT 660  
 DB 782 ACTCAGCAGCAGGTTCACATTTCTCTTGAAGATTAAAGAACAGGAAAGCTTCAGACTT 841  
 QY 661 CTGAACCCCATCTCTAAGCCAAACCCCAAAACAACTGA 699  
 DB 842 CTGAACCCCATCTCTAAGCCAAACCCCAAAACAACTGA 880  
 XX RESULT 10  
 XX AAF24912/c  
 XX ID AAF24912 standard; DNA; 1198 BP.  
 XX AC AAF24912;  
 XX DT 30-APR-2001 (first entry)  
 XX DE Complement sequence of a human Fc epsilon receptor alpha-chain gene.  
 XX KW Fc epsilon receptor; FcεpsilonR; immunoglobulin E; IgE; atopic disease;  
 XX KW luminescence inducing protein; allergy; hyper IgE syndrome;  
 XX KW internal parasite infection; B cell neoplasia; ss.  
 XX OS Homo sapiens.  
 XX PN WO200104310-A1.  
 XX PD 18-JAN-2001.  
 XX PF 13-JUL-2000; 2000WO-US019070.  
 XX PR 13-JUL-1999; 99US-0143612P.  
 XX PR 02-MAR-2000; 2000US-0186412P.  
 XX PA (HESK-) HESKA CORP.  
 XX PA (PROM-) PROMEGA CORP.  
 XX PI Weber ER, Wood KV, Hall MP;  
 XX WPI; 2001-103082/11.  
 XX A fusion protein, comprising an Fc epsilon receptor domain and a luminescence inducing protein domain that induces a LP substrate to emit light when contacted with the LP domain, useful for detecting immunoglobulin (Ig) E.  
 XX Example; Page 61; 105pp; English.  
 XX The present sequence represents the complement of a human Fc epsilon receptor (FcεpsilonR) alpha-chain protein, that binds to immunoglobulin (Ig) E. The FcεpsilonR domain is used to produce a fusion protein, which also comprises a luminescence inducing protein domain that induces a substrate to emit light when contacted with the luminescence inducing protein domain. The fusion protein may be used to detect IgE. It may also be used to identify a compound capable of inhibiting FcεpsilonR protein activity. IgE antibody production is indicative of diseases such as allergies, atopic disease, hyper IgE syndrome, internal parasite infections, and B cell neoplasia. Detection of IgE production in an animal following therapy is indicative of the efficacy of the treatment, for example when using treatments intended to disrupt IgE production  
 XX SQ Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 699; DB 5; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 DB 1017 GTCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 958

QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
DB 957 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 898  
QY 121 CACAAATGGAGGCTTTGAG 180  
DB 897 CACAAATGGAGGCTTTGAG 838  
QY 181 GAAGACAGTGGAGAGATACAAATGTCAGACCAACCAAGTTAATCAGAGTGAACCTGTGTAC 240  
DB 837 GAAGACAGTGGAGAGATACAAATGTCAGACCAACCAAGTTAATCAGAGTGAACCTGTGTAC 778  
QY 241 CTGGAAGTCTTACAGTACCTGCTCTTCAAGGCTCTGCTGAGAGTGGTGTGAGAGGCG 300  
DB 777 CTGGAAGTCTTACAGTACCTGCTCTTCAAGGCTCTGCTGAGAGTGGTGTGAGAGGCG 718  
QY 301 CAGCCCTCTTCTCAGGTCGCAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 717 CAGCCCTCTTCTCAGGTCGCAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACCAATCTCCATTACAAAT 420  
DB 657 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACCAATCTCCATTACAAAT 598  
QY 421 GCCACAGTTGAAGACAGTGGAGCTTACTGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 597 GCCACAGTTGAAGACAGTGGAGCTTACTGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 538  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGCGTGAGAGAGTACTGGCTACAA 540  
DB 537 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGCGTGAGAGAGTACTGGCTACAA 478  
QY 541 TTTTATCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600  
DB 477 TTTTATCCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 418  
QY 601 ACTCAGCAGTGCATCTTCTTTGAAGATTAAGAGAACCAAGAGAGAGAGAGAGAGAGAG 660  
DB 417 ACTCAGCAGTGCATCTTCTTTGAAGATTAAGAGAACCAAGAGAGAGAGAGAGAGAGAG 358  
QY 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACCAACTGA 699  
DB 357 CTGAACCCCATCTTAAGCCAAACCCCAAAACCAACTGA 319

RESULT 11  
ID AAF24911 standard; DNA; 1198 BP.  
XX AAF24911;  
AC AAF24911;  
XX AAF24911;  
DT 30-APR-2001 (first entry)  
XX Nucleotide sequence of a human Fc epsilon receptor alpha-chain.  
DE Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;  
XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;  
KW luminescence inducing protein; allergy; hyper IgE syndrome;  
KW internal parasite infection; B cell neoplasia; SS.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Key Location/Qualifiers  
XX CDS 107..880  
FT /\*tag= a  
FT /product= "Fc epsilon receptor alpha-chain"  
XX  
XX WO200104310-A1.  
XX  
XX 18-JAN-2001.  
XX  
XX 13-JUL-2000; 2000WO-US019070.  
XX

PR 13-JUL-1999; 99US-0143612P.  
PR 02-MAR-2000; 2000US-0186412P.  
PA (HESK-) HESKA CORP.  
PA (PROM-) PROMEGA CORP.  
XX Weber ER, Wood KV, Hall MP;  
PI WPI; 2001-103082/11.  
XX P-PSDB; AAB31584.  
DR A fusion protein, comprising an Fc epsilon receptor domain and a  
PT luminescence inducing protein domain that induces a LP substrate to emit  
PT light when contacted with the LP domain, useful for detecting  
PT immunoglobulin (Ig) E.  
XX Claim 17; Page 58-59; 105pp; English.  
PS The present sequence encodes a human Fc epsilon receptor (Fc epsilonR)  
XX alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilonR  
CC domain is used to produce a fusion protein, which also comprises a  
CC domain inducing protein domain that induces a substrate to emit  
CC luminescence inducing protein domain. The fusion protein may be used to  
CC light when contacted with the luminescence inducing protein domain. The  
CC fusion protein may be used to detect IgE. It may also be used to identify  
CC a compound capable of inhibiting Fc epsilonR protein activity. IgE  
CC antibody production is indicative of diseases such as allergies, atopic  
CC disease, hyper IgE syndrome, internal parasite infections and B cell  
CC neoplasia. Detection of IgE production in an animal following therapy is  
CC indicative of the efficacy of the treatment, for example when using  
CC treatments intended to disrupt IgE production  
XX  
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
Query Match 100.0%; Score 699; DB 5; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;  
Matches 699; Conservative 0; Mismatches 0;  
QY 1 GTCCTCTCAGAAACCTTAAGTCTCTTGAACCTCTCCATGGAATAGAAATTTAAAGGAGAG 60  
DB 182 GTCCTCTCAGAAACCTTAAGTCTCTTGAACCTCTCCATGGAATAGAAATTTAAAGGAGAG 241  
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
DB 242 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301  
QY 121 CACAAATGGAGGCTTTGAG 180  
DB 302 CACAAATGGAGGCTTTGAG 361  
QY 181 GAAGACAGTGGAGAGATACAAATGTCAGACCAACCAAGTTAATCAGAGTGAACCTGTGTAC 240  
DB 362 GAAGACAGTGGAGAGATACAAATGTCAGACCAACCAAGTTAATCAGAGTGAACCTGTGTAC 421  
QY 241 CTGGAAGTCTTCAAGTACCTGCTCTTCAAGGCTCTGCTGAGGTCGTTGATGGAGGCG 300  
DB 422 CTGGAAGTCTTCAAGTACCTGCTCTTCAAGGCTCTGCTGAGGTCGTTGATGGAGGCG 481  
QY 301 CAGCCCTCTTCTCAGGTCGCAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
DB 482 CAGCCCTCTTCTCAGGTCGCAATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACCAATCTCCATTACAAAT 420  
DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAACCAATCTCCATTACAAAT 601  
QY 421 GCCACAGTTGAAGACAGTGGAGCTTACTGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
DB 602 GCCACAGTTGAAGACAGTGGAGCTTACTGTTAGAGAGAGAGAGAGAGAGAGAGAGAG 661  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGCGTGAGAGAGTACTGGCTACAA 540  
DB 662 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCTCCGCGTGAGAGAGTACTGGCTACAA 721

QY 541 TTTTATCCCATCTTGGTGTGATCTGTTTCTGTGGACACAGGATTATTTATCTCA 600  
 DB 722 TTTTATCCCATCTTGGTGTGATCTGTTTCTGTGGACACAGGATTATTTATCTCA 781  
 QY 601 ACTGACGACGAGTCACTTTCTCTTGAAGATTAAAGAGAACACGAAAGGCTTCAGACTT 660  
 DB 782 ACTGACGACGAGTCACTTTCTCTTGAAGATTAAAGAGAACACGAAAGGCTTCAGACTT 841  
 QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
 DB 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880

## RESULT 12

ABL67793  
 ID ABL67793 standard; DNA; 1198 BP.  
 XX  
 AC ABL67793;  
 XX  
 DT 15-MAY-2002 (first entry)  
 XX  
 DE Oesophagus cancer related gene sequence SEQ ID NO:6130.  
 XX  
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
 KW gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200194629-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 30-MAY-2001; 2001WO-US010838.  
 XX

PR 03-OCT-2000; 2000US-0237604P.  
 PR 03-OCT-2000; 2000US-0237606P.  
 PR 03-OCT-2000; 2000US-0237608P.  
 PR 01-NOV-2000; 2000US-0244867P.  
 PR 01-NOV-2000; 2000US-0245084P.  
 XX  
 PA (AVAL-) AVALON PHARM.  
 XX  
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 PI  
 XX WPI; 2002-189264/24.  
 DR  
 XX  
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical  
 PT agent to be tested for anti-neoplastic activity, and determining a change  
 PT in expression of a gene of a signature gene set.  
 XX  
 XX Claim 1; SEQ ID NO 6130; 44pp; English.  
 PS  
 XX  
 CC The present invention describes a method (M1) for screening for an anti-  
 CC neoplastic agent. The method involves exposing cells to a chemical agent  
 CC to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening an  
 CC anti-neoplastic agent, and can be used for producing a product which is  
 CC of M1, and the data is sufficient to convey the chemical structure and/or  
 CC properties of the agent. M1 can be used in the treatment of cancer such  
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
 CC tumour  
 CC  
 XX Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 699; DB 6; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 60  
 DB 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGATAGATATTTAAAGGAGAG 241  
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120  
 DB 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 301  
 QY 121 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTGTGATATTTGATGCCAAATTT 180  
 DB 302 CACATGGCAGCCTTTCAGAGAGACAAATTCAGATTGTGATATTTGATGCCAAATTT 361  
 QY 181 GAAGACAGTGGAGATACAAATGTCCAGCACCACCAAGTTAATGAGATGAACCTGTGTAC 240  
 DB 362 GAAGACAGTGGAGATACAAATGTCCAGCACCACCAAGTTAATGAGATGAACCTGTGTAC 421  
 QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTTTCAGGCTCTGCTGAGGTGGTGGATGGAGGC 300  
 DB 422 CTGGAAGTCTTTCAGTGAAGTCTCTTTCAGGCTCTGCTGAGGTGGTGGATGGAGGC 481  
 QY 301 CAGCCCTCTTCTCCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAGGTGATCTAT 360  
 DB 482 CAGCCCTCTTCTCCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAGGTGATCTAT 541  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420  
 DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 601  
 QY 421 GCCACAGTTGAGACAGTGGACCTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 480



Db 602 GCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 661  
Qy 481 GAGCTGACGCCCTCAACATTACTGTATAAAGCTCCGCGTCAAGACTGCTGCTACAA 540  
Db 662 GAGCTGACGCCCTCAACATTACTGTATAAAGCTCCGCGTCAAGACTGCTGCTACAA 721  
Qy 541 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 600  
Db 722 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 781  
Qy 601 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACACAGGAAGCTTCAGACTT 660  
Db 782 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACACAGGAAGCTTCAGACTT 841  
Qy 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699  
Db 842 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 13  
ABZ96629  
ID ABZ96629 standard; DNA; 1198 BP.  
XX  
AC ABZ96629;  
XX  
DT 17-OCT-2003 (first entry)  
XX  
DE Human high affinity IgE receptor oligonucleotide fragment.  
XX  
KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
KW lung inflammation; respiratory disease; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200285308-A2.  
XX  
XX 31-OCT-2002.  
XX  
XX 23-APR-2002; 2002WO-US013135.  
XX  
XX 24-APR-2001; 2001US-0286137P.  
XX  
XX (EPIG-) EPIGENESIS PHARM INC.  
XX  
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahabuddin S;  
XX  
XX WPI; 2003-229219/22.  
XX

Pharmaceutical composition for treating ailments associated with impaired  
respiration, has oligo(s) antisense to specific gene(s) or its  
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
ubiquinone.  
XX  
PS Disclosure; SEQ ID NO 11871; 872pp; English.  
XX  
XX The invention relates to a novel pharmaceutical composition, which has a  
CC first active agent comprising an oligonucleotide antisense to the  
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
CC junctions of genes encoding a polypeptide associated with lung and/or  
CC nasal airway dysfunction and a second active agent comprising an  
CC antiinflammatory steroid and ubiquinone. A composition of the invention  
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
CC immunosuppressive, and cytostatic activity. The composition may have a  
CC use in antisense gene therapy. The composition is useful for treating or  
CC preventing a respiratory, lung or malignant disease or condition, also  
CC for enhancing the prophylactic or therapeutic respiratory effect of an  
CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
CC lung inflammation, lung allergies, or a respiratory disease or condition.  
CC Note: the sequence data for this patent is not represented in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query March 100.0%; Score 699; DB 7; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 7.1e-200; Indels 0; Gaps 0;  
Matches 699; Conservative 0; Mismatches 0;  
Qy 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTAAAGGAGAG 60  
Db 182 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTAAAGGAGAG 241  
Qy 61 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCACCAATGCTTC 120  
Db 242 AATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGTTCACCAATGCTTC 301  
Qy 121 CACAATGCGAGCCCTTTCAGAAAGACACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180  
Db 302 CACAATGCGAGCCCTTTCAGAAAGACACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 361  
Qy 181 GAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421  
Qy 241 CTGGAAGTCCTCAGTGTGCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 300  
Db 422 CTGGAAGTCCTCAGTGTGCTGCTCTCTTCAGAGCCCTCTGCTGAGGTGGTGTATGGAGGGC 481  
Qy 301 CAGCCCTCTTCTCTCAGTGTGCTGCTGCTGCTGAGGAACTGGGATGTTACAAGGTGATCTAT 360  
Db 482 CAGCCCTCTTCTCTCAGTGTGCTGCTGCTGCTGAGGAACTGGGATGTTACAAGGTGATCTAT 541  
Qy 361 TATAAGGATGTGAAAGCTCTCAAGTACTGTATGAGAACCAACACATCTCCATTACAAAT 420  
Db 542 TATAAGGATGTGAAAGCTCTCAAGTACTGTATGAGAACCAACACATCTCCATTACAAAT 601  
Qy 421 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
Db 602 GCCACAGTTGAAGACAGTGGAAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 661  
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTACAA 540  
Db 662 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCGTGAAGAGTACTGGCTACAA 721  
Qy 541 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 600  
Db 722 TTTTATCCCATTTGTTGGTGTGATTCTGTTGCTGTGGACACAGGATTATTATCTCA 781  
Qy 601 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACACAGGAAGCTTCAGACTT 660  
Db 782 ACTCAGCAGAGTCACTTTCTTTGAAGATTAGAGAACACAGGAAGCTTCAGACTT 841  
Qy 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699  
Db 842 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 14  
ABZ85535  
ID ABZ85535 standard; cDNA; 1198 BP.  
XX  
AC ADB85535;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Human immunoglobulin E high affinity receptor (FcERI) alpha subunit cDNA.  
XX

KW alpha subunit; high affinity receptor for immunoglobulin E; FCERI;  
 KW mast cell; basophil; histamine; serotonin; allergic condition;  
 KW antiallergic; allergic response; drug screening assay; immunoglobulin E;  
 KW human; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT CDS 107..880  
 FT /tag= a  
 FT /product= "Human FCERI receptor"  
 FT /transl\_except= (767..769, aa:Glu)  
 FT /transl\_except= (863..865, aa:Asp)  
 XX  
 XX US6602983-B1.  
 XX  
 XX 05-AUG-2003.  
 XX  
 XX 22-SEP-1994; 94US-00310902.  
 XX  
 XX 24-FEB-1988; 88US-00160457.  
 PR 30-OCT-1991; 91US-00785127.  
 PR 29-MAY-1993; 93US-00066640.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Kinet JP, Kochan JP;  
 XX  
 XX WPI; 2003-669612/63.  
 DR P-PSDB; ADB85536.  
 XX  
 XX New alpha subunit of the human high affinity receptor for immunoglobulin  
 FT E polypeptides, useful as antagonists to prevent allergic response, as  
 FT reagents in drug screening assays, or for monitoring immunoglobulin E  
 FT levels in patients.  
 XX  
 XX Claim 1; Fig 1; 9pp; English.  
 XX  
 XX This invention relates to a novel purified polypeptide corresponding to  
 CC the alpha subunit of the human high affinity receptor for immunoglobulin  
 CC E (FcERI) and the DNA sequence which encodes it. The receptor of the  
 CC invention is found exclusively on mast cells, basophils and related  
 CC cells. Activation of the receptor triggers the release of preformed  
 CC mediators such as histamine and serotonin which may result in allergic  
 CC conditions. Compounds which modulate FCERI activity may have an antiallergic  
 CC activity. The polypeptide of the invention may be useful as an antagonist  
 CC for preventing allergic response, as a reagent in drug screening assays,  
 CC as a therapeutic or for monitoring immunoglobulin E levels in patients.  
 CC The DNA sequences may be useful for producing the polypeptide or for  
 CC synthesising cDNA sequences to construct DNA probes used in diagnostic  
 CC assays. The present sequence is the cDNA sequence encoding the alpha  
 CC subunit of the human FCERI receptor of the invention.  
 XX  
 XX Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 699; DB 9; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-200;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60  
 DB 182 GTCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 241  
 QY 61 AATGTGACTCTTACATGTATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120  
 DB 242 AATGTGACTCTTACATGTATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGGTTC 301  
 QY 121 CACAATGGCAGCTTTTCAGAAAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 180  
 DB 302 CACAATGGCAGCTTTTCAGAAAGACAAATTTCAAGTTTGAATTTGTAATGCCAAATTT 361  
 QY 181 GAAGACAGTGGAGAAATCAAAATGTGACACCAACAAATTTAATGAGAGTGAACCTGTGTAC 240

DB 362 GAAGACAGTGGAGAAATCAAAATGTGACACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 421  
 QY 241 CTGGAAGTCTTCAGTGAATGGCTGCTCTCTTCAAGGCTCTGCTGAGGTGGTGAAGGGC 300  
 DB 422 CTGGAAGTCTTCAGTGAATGGCTGCTCTCTTCAAGGCTCTGCTGAGGTGGTGAAGGGC 481  
 QY 301 CAGCCCTCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360  
 DB 482 CAGCCCTCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 541  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACCAATCTCCATTACAAT 420  
 DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACCAATCTCCATTACAAT 601  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 480  
 DB 602 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGACTAT 661  
 QY 481 GAGTCTGAGCCCTCTCAACATTTACTGTATATAAAGCTCCGCTGAGAACTACTGGCTACAA 540  
 DB 662 GAGTCTGAGCCCTCTCAACATTTACTGTATATAAAGCTCCGCTGAGAACTACTGGCTACAA 721  
 QY 541 TTTTATCCCATTTGTTGGTGGTGAATCTCTGTTGCTGTGGACACAGATTTATTTATCTCA 600  
 DB 722 TTTTATCCCATTTGTTGGTGGTGAATCTCTGTTGCTGTGGACACAGATTTATTTATCTCA 781  
 QY 601 ACTCAGCAGCAGGTCAACATTTCTTCTTGAAGATTAAAGAACCAAGGCTTCAGACTT 660  
 DB 782 ACTCAGCAGCAGGTCAACATTTCTTCTTGAAGATTAAAGAACCAAGGCTTCAGACTT 841  
 QY 661 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACCAACTGA 699  
 DB 842 CTGAACCCCATCTCTTAAGCCAAACCCCAAAACCAACTGA 880  
 XX  
 XX RESULT 15  
 XX AAA34816  
 XX ID AAA34816 standard; DNA; 21742 BP.  
 XX AC AAA34816;  
 XX XX  
 XX DT 28-JUL-2000 (first entry)  
 XX XX  
 XX DE Human adenosine receptor related polynucleotide SEQ ID NO:2505.  
 XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN WO200009525-A2.  
 XX  
 XX PD 24-FEB-2000.  
 XX  
 XX PF 03-AUG-1999; 99WO-US017712.  
 XX  
 XX PR 03-AUG-1998; 98US-0095212P.  
 XX  
 XX PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX PI Nyce JW;  
 XX  
 XX DR WPI; 2000-205971/18.  
 XX  
 XX PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or  
 PT bronchitis, emphysema, respiratory distress syndrome, ischaemia or



```

Db      9074      TTTTATCCCATTTGTTGGTGTGATCTCTGTTGCTGTGGACACAGGATTATTTATCTCA  9133
Qy      601      ACTCAGCAGCAGTGCACATTTCTCTTGAAGATTAAAGAGAACCGAGGAAGGCTTCAGACTT  660
Db      9134      ACTCAGCAGCAGTGCACATTTCTCTTGAAGATTAAAGAGAACCGAGGAAGGCTTCAGACTT  9193
Qy      661      CTGAACCCCATCTCTAAGCCAAACCCCAAAAAACAATGA  699
Db      9194      CTGAACCCCATCTCTAAGCCAAACCCCAAAAAACAATGA  9232

Search completed: October 8, 2004, 23:17:39
Job time : 340.879 secs

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PT	cancers.
XX	Disclosure; Page 659-664; 1343pp; English.
XX	The present invention describes a new composition comprising an antisense
XX	oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC	nucleic acids involved in bronchoconstriction, allergies, and/or
CC	inflammation. The ON can have antiinflammatory, antiallergic,
CC	antiasthmatic, cytostatic and analgesic activities. The compositions are
CC	useful for the treatment of diseases associated with inflammation,
CC	impaired airways, including lung disease and diseases whose secondary
CC	effects afflict the lungs of a subject. They can be used for treating
CC	e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC	impaired respiration, respiratory distress syndrome, pain, cystic
CC	fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC	pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
CC	carcinomas, and cancers which may metastasize to the lungs, including
CC	breast and prostate cancer. The reduction of the adenosine content of the
CC	ONs reduces side effects. The A-containing ONs break down with the
CC	release of deoxyadenosine which activates adenosine receptors causing
CC	bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC	nucleotide sequences given in the sequence listing from the present
CC	invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC	sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC	from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC	AAA33932) are specifically claimed ONs from the present invention. N.B.
CC	Sequences given in the disclosure of the present invention do not match
CC	up with their corresponding SEQ ID NO: sequences given in the sequence
CC	listing
XX	
XX	Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;
XX	Query Match 100.0%; Score 699; DB 3; Length 21742;
XX	Best Local Similarity 100.0%; Pred. No. 3,1e-199;
XX	Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTCCCTCAGAAACCTTAGTGCTCTTGAAACCTTCCTAGGAATAGAAATATTTAAAGGAGAG 60
DB	8534 GTCCCTCAGAAACCTTAGTGCTCTTGAAACCTTCCTAGGAATAGAAATATTTAAAGGAGAG 8593
QY	61 AATGTGACTCTTACATGTAATGGGAAACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
DB	8594 AATGTGACTCTTACATGTAATGGGAAACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 8653
QY	121 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATGTGAATGCCAAATTT 180
DB	8654 CACAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATGTGAATGCCAAATTT 8713
QY	181 GAAGCAGTGGAGATACAAATGTGCAGCCACCAAGTTAATCAGAGTGAACCTGTGTAC 240
DB	8714 GAAGCAGTGGAGAAATACAAATGTGCAGCCACCAAGTTAATCAGAGTGAACCTGTGTAC 8773
QY	241 CTGGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGCCCTCTGCTGAGTGGTGTAGGAGGC 300
DB	8774 CTGGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGCCCTCTGCTGAGTGGTGTAGGAGGC 8833
QY	301 CAGCCCTCTCTCAGTGGCCATGGTTGGAGNACTGGGATGTGTACAGCTGATCTAT 360
DB	8834 CAGCCCTCTCTCAGTGGCCATGGTTGGAGNACTGGGATGTGTACAGCTGATCTAT 8893
QY	361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATCAGAAACCAACCAATCTCCATTACAAT 420
DB	8894 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATCAGAAACCAACCAATCTCCATTACAAT 8953
QY	421 GCCACAGTTGAAGAAGTGGAACTTACTCTGTAACGGGAAAAGTGTGGCAGCTGACTAT 480
DB	8954 GCCACAGTTGAAGAAGTGGAACTTACTCTGTAACGGGAAAAGTGTGGCAGCTGACTAT 9013
QY	481 GAGTCTGACCCCTCAACATTACTGTAAATAAAGCTCCGCGTGGAAAGTACTGGCTACAA 540
DB	9014 GAGTCTGACCCCTCAACATTACTGTAAATAAAGCTCCGCGTGGAAAGTACTGGCTACAA 9073
QY	541 TTTTATATCCCAATGTTGGTGGTGATCTCTGTTGCTGTGGACACACAGATTTTATPCTCA 600

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 61.7962 Seconds  
(without alignments)  
6277.259 Million cell updates/sec

Title: US-10-763-400-7  
Perfect score: 699  
Sequence: 1 gtcctcagaaccttaaggt.....caaaccccaaaactga 699

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Capext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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5: /cgn2\_6/prodata/2/ina/PCUTUS\_COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699	100.0	699	2	US-08-756-387B-7
2	699	100.0	699	4	US-09-285-873-7
3	699	100.0	699	4	US-09-944-277A-7
4	699	100.0	774	2	US-08-756-387B-4
5	699	100.0	774	2	US-08-756-387B-5
6	699	100.0	774	4	US-09-285-873-4
7	699	100.0	774	4	US-09-285-873-5
8	699	100.0	774	4	US-09-944-277A-4
9	699	100.0	774	4	US-09-944-277A-5
10	699	100.0	1174	1	US-07-869-933-10
11	699	100.0	1174	3	US-09-103-663-10
12	699	100.0	1198	2	US-08-756-387B-1
13	699	100.0	1198	2	US-08-756-387B-3
14	699	100.0	1198	4	US-09-285-873-1
15	699	100.0	1198	4	US-09-285-873-3
16	699	100.0	1198	4	US-09-944-277A-1
17	699	100.0	1198	4	US-09-944-277A-3
18	698	99.9	773	4	US-08-897-556A-6
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20	516	73.8	516	2	US-08-756-387B-12
21	516	73.8	516	4	US-09-285-873-12
22	516	73.8	516	4	US-09-944-277A-12
23	516	73.8	591	2	US-08-756-387B-10
24	516	73.8	591	4	US-09-285-873-10
25	516	73.8	591	4	US-09-944-277A-10
26	516	73.8	713	2	US-08-238-027-3
27	514.4	73.6	591	3	US-08-788-954-1

28	395.8	56.6	1015	3	US-09-015-734-1	Sequence 1, Appli
c 29	395.8	56.6	1015	3	US-09-015-734-3	Sequence 3, Appli
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c 31	395.8	56.6	1015	4	US-09-515-311-3	Sequence 3, Appli
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c 33	392.4	56.1	708	3	US-09-015-734-8	Sequence 8, Appli
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c 35	392.4	56.1	708	4	US-09-515-311-8	Sequence 8, Appli
36	392.4	56.1	765	3	US-09-015-734-5	Sequence 5, Appli
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c 41	376.4	53.8	1069	2	US-08-768-964-3	Sequence 3, Appli
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c 43	376.4	53.8	1069	3	US-09-005-299-3	Sequence 3, Appli
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c 45	376.4	53.8	1069	3	US-09-515-431-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-756-387B-7  
; Sequence 7, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 699 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..699  
US-08-756-387B-7

Query Match 100.0%; Score 699; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 1.5e-221;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTCCCTCAGAACCTTAAGGTCTTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60

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DB 121 CACAATGGCAGCTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCGCAAAATTT 180

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DB 361 TATAAGGATGGTGAAGTCTTCAGTGAAGTCTTCCTTCAAGTCTGCTCAGGCTCTGCTGAGTGGTGAAGGCG 300

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QY 601 ACTCAGCAGCAGTGCACATTTCTTGAAGTCTGCTGAGTGGTGAAGGCG 300
DB 601 ACTCAGCAGCAGTGCACATTTCTTGAAGTCTGCTGAGTGGTGAAGGCG 300

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## RESULT 2

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US-09-285-873-7
; Sequence 7, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:

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; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95

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; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: NO. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; US-09-285-873-7

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Query Match 100.0%; Score 699; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.5e-211;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTCCCTCAGAACCTTAAGGTCTTCCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATATGTTTC 120

QY 121 CACAATGGCAGCTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCGCAAAATTT 180
DB 121 CACAATGGCAGCTTTCAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCGCAAAATTT 180

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DB 361 TATAAGGATGGTGAAGTCTTCAGTGAAGTCTTCCTTCAAGTCTGCTCAGGCTCTGCTGAGTGGTGAAGGCG 300

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DB 421 GCCCAGTGGAGACAGTGGAACTTCTTGAAGTCTGCTGAGTGGTGAAGGCG 300

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RESULT 3  
US-09-944-277A-7  
; Sequence 7, Application US/09944277A  
; Patent No. 6682894  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 699 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..699  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-944-277A-7

Query Match 100.0%; Score 699; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 1.5e-221;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AATGTGACTTCTACATGTAATGGAAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120

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Db 121 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATATGTAATGCAATTT 180

QY 181 GAAGACAGTGGGAATACAAATGTCTCAGCACCAACAACTTAATGAGAGTGAACTGTGTAC 240  
Db 181 GAAGACAGTGGGAATACAAATGTCTCAGCACCAACAACTTAATGAGAGTGAACTGTGTAC 240

QY 241 CTGGAAGTCTTTCAGTGTCTCTCTTTCAGCCCTCTCTCTGAGTGTGTGAGAGGC 300  
Db 241 CTGGAAGTCTTTCAGTGTCTCTCTTTCAGCCCTCTCTCTGAGTGTGTGAGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGTCTCTCTTTCAGCCCTCTCTCTGAGTGTGTGAGAGGC 360  
Db 301 CAGCCCTCTTCTCAGTGTCTCTCTTTCAGCCCTCTCTCTGAGTGTGTGAGAGGC 360

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTGAGAACCAACCAATCTCTCAATACAAAT 420  
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTGAGAACCAACCAATCTCTCAATACAAAT 420

QY 421 GCCACAGTTGAAGACAGTGGAACTTACTTCTGAGGGAAGAGTGTGAGAGTGGAGTAT 480  
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTTCTGAGGGAAGAGTGTGAGAGTGGAGTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTACTTAAAGCTCCGCTGAGAAAGTACTGCTGCTACAA 540  
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QY 541 TTTTATCCCATTTGTTGGTGTCTCTGTTTCTGAGACACAGGATTTATTTCTCA 600  
Db 541 TTTTATCCCATTTGTTGGTGTCTCTGTTTCTGAGACACAGGATTTATTTCTCA 600

QY 601 ACTCAGCAGCGTCACTTTCTTGAAGATTAAAGAACACGGAAGGCTTCAGACTT 660  
Db 601 ACTCAGCAGCGTCACTTTCTTGAAGATTAAAGAACACGGAAGGCTTCAGACTT 660

QY 661 CTGAACCCCACTCTTAAGCCAAACCCCAAACTGA 699  
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RESULT 4  
US-08-756-387B-4  
; Sequence 4, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESS: Heskia Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-08-756-387B-4

Query Match      100.0%; Score 699; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 76 GTCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGATAGATAATTTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 195
QY 121 CACAATGGCAGCCTTTGAGAAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 180
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QY 241 CTGAAGTCTTCAGTGAAGTGGTCTCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db 316 CTGAAGTCTTCAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 375
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Db 376 CAGCCCTCTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 435
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Db 436 TATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495
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Db 496 GCCACAGTTGAAGCAGTGGAACTTACTACTGACGGGCAAGTGGGAGCTGGACTAT 555
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGTCTCCGGTGGAGAGTACTGGCTACAA 540
Db 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGTCTCCGGTGGAGAGTACTGGCTACAA 615
QY 541 TTTTATATCCATTTGGTGGTGAATCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 600
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## RESULT 5

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US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.

```

```

; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-756-387B-5

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Query Match      100.0%; Score 699; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGATAGATAATTTAAAGGAGAG 60
Db 699 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGATAGATAATTTAAAGGAGAG 640
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120
Db 639 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 580
QY 121 CACAATGGCAGCCTTTGAGAAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 180
Db 579 CACAATGGCAGCCTTTGAGAAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 520
QY 181 GAAGACAGTGGAGAAATCAAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 519 GAAGACAGTGGAGAAATCAAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 460
QY 241 CTGAAGTCTTCAGTGAAGTGGTCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db 459 CTGAAGTCTTCAGTGAAGTGGTCTCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGG 400
QY 301 CAGCCCTCTCTCAGTGGCCTATGGTGGAGAACTGGGATGTGTACAAGGTGATCTAT 360
Db 399 CAGCCCTCTCTCAGTGGCCTATGGTGGAGAACTGGGATGTGTACAAGGTGATCTAT 340
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCTCATTTACAAAT 420
Db 339 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCTCATTTACAAAT 280
QY 421 GCCACAGTTGAAGCAGTGGAACTTACTACTGTCAGGGCAAGTGGCAGCTGGACTAT 480
Db 279 GCCACAGTTGAAGCAGTGGAACTTACTACTGTCAGGGCAAGTGGCAGCTGGACTAT 220
QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCTCCGGTGGAGAGTACTGGCTACAA 540

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-285-873-5

Query Match 100.0%; Score 699; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 60
DB 699 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 640

QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
DB 639 AATGTGACTTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 580

QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 180
DB 579 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 520

QY 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAACTGATGATGAGAGTGAATCTGTAC 240
DB 519 GAAGACAGTGGAGATACAAATGTCAGACCAACAACTGATGATGAGAGTGAATCTGTAC 460

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGCCCTCTCTGAGGTGGTGGAGGGC 300
DB 459 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGCCCTCTCTGAGGTGGTGGAGGGC 400

QY 301 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACTGGGATGTTACAGAGGTGATCTAT 360
DB 399 CAGCCCTCTTCTCAGTGCATGTTGGAGGAACTGGGATGTTACAGAGGTGATCTAT 340

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
DB 339 TATAAGGATGGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 280

QY 421 GCCACAGTGGAGACAGTGGAACTACTACTGACGGGCAAGTGTGGAGCTGGACTAT 480
DB 279 GCCACAGTGGAGACAGTGGAACTACTACTGACGGGCAAGTGTGGAGCTGGACTAT 220

QY 481 GAGTCTGAGCCCTTCAACATTTACTGTATATAAAGCTCCGCGTGAGAGTACTGGCTACAA 540
DB 219 GAGTCTGAGCCCTTCAACATTTACTGTATATAAAGCTCCGCGTGAGAGTACTGGCTACAA 160

QY 541 TTTTATATCCATGTTGGTGGATTTCTGTTGCTGTGGACACAGGATATTATCTCA 600
DB 159 TTTTATATCCATGTTGGTGGATTTCTGTTGCTGTGGACACAGGATATTATCTCA 100

QY 601 ACTCAGCAGAGGTGCATTTCTCTCAAGATTAAAGAACACAGGAAAGCTTCAGACTT 560
DB 99 ACTCAGCAGAGGTGCATTTCTCTGAGATTAAAGAACACAGGAAAGCTTCAGACTT 40

QY 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699
DB 39 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 1
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RESULT 8
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; PORTER, James P.
; RUSHLOW, Keith E.
; WASSOM, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4
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Query Match 100.0%; Score 699; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.6e-221;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 60
DB 76 GTCCTCAGAACCTAAGTCTCTTGAACCTCCATGGAAATGAATATTAAAGGAG 135

QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120
DB 136 AATGTGACTTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 195

QY 121 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 180
DB 196 CACATGGCAGCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCAATTT 255

QY 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAACTGATGATGAGAGTGAATCTGTAC 240
DB 256 GAAGACAGTGGAGATACAAATGTCAGACCAACAACTGATGATGAGAGTGAATCTGTAC 315

QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTCAAGCCCTCTCTGAGGTGGTGGAGGGC 300
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Db 316 CTGGAAGTCTTCAGTGAGTGGTCTCTCTTCAAGCCCTCTGCTGAGGTGGTATGAGGGC 375  
Qy 301 CAGCCCTCTCTCAGTGGTCCATGGTGGAGAACTGGGATGTGTACAGGTGATCTAT 360  
Db 376 CAGCCCTCTCTCAGTGGTCCATGGTGGAGAACTGGGATGTGTACAGGTGATCTAT 435  
Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420  
Db 436 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 495  
Qy 421 GCACAGTGTGAAGACAGTGAACCTTACTACTGTGTACGGGCAAGTGTGGAGCTGACTAT 480  
Db 496 GCCACAGTGTGAAGACAGTGAACCTTACTACTGTGTACGGGCAAGTGTGGAGCTGACTAT 555  
Qy 481 GAGTCTGAGCCCTCAACATCTACTGTGTATGAGAACCAACATCTCCATTACAAAT 540  
Db 556 GAGTCTGAGCCCTCAACATCTACTGTGTATGAGAACCAACATCTCCATTACAAAT 615  
Qy 541 TTTTATCCATTTGTTGGTGTATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 600  
Db 616 TTTTATCCATTTGTTGGTGTATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 675  
Qy 601 ACTCAGCAGAGTGCATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 660  
Db 676 ACTCAGCAGAGTGCATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 735  
Qy 661 CTGAACCCACATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 699  
Db 736 CTGAACCCACATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 774

RESULT 9  
US-09-944-277A-5/c  
; Sequence 5, Application US/09944277A  
; Patent No. 6682894  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 nucleotides  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-944-277A-5  
Query Match 100.0%; Score 699; DB 4; Length 774;  
Best Local Similarity 100.0%; Pred. No. 1.6e-221;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60  
Db 699 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 640  
Qy 61 AATGTGACTCTTACATGTAAATGGGAACAAATTTCTTTGAAGTCAGTTCCACAAATGPTC 120  
Db 639 AATGTGACTCTTACATGTAAATGGGAACAAATTTCTTTGAAGTCAGTTCCACAAATGPTC 580  
Qy 121 CCAATGAGAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCCAAATTT 180  
Db 579 CCAATGAGAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCCAAATTT 520  
Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 519 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 460  
Qy 241 CTGGAAGTCTTCAAGTGTGCTCTTCAAGTGTGCTCTTCAAGTGTGCTCTTCAAGTGTGCTCT 300  
Db 459 CTGGAAGTCTTCAAGTGTGCTCTTCAAGTGTGCTCTTCAAGTGTGCTCTTCAAGTGTGCTCT 400  
Qy 301 CAGCCCTCTTCTCAGTGGTCCATGGTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360  
Db 399 CAGCCCTCTTCTCAGTGGTCCATGGTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 340  
Qy 361 TATAAGGATGGTGAAGCTCTCAAGTGTGATGAGAACCAACATCTCCATTACAAAT 420  
Db 339 TATAAGGATGGTGAAGCTCTCAAGTGTGATGAGAACCAACATCTCCATTACAAAT 280  
Qy 421 GCCACAGTGAAGACAGTGGACCTTACTACTGTAGCGGCAAGTGTGGAGCTGAGCTAT 480  
Db 279 GCCACAGTGAAGACAGTGGACCTTACTACTGTAGCGGCAAGTGTGGAGCTGAGCTAT 220  
Qy 481 GAGTCTGAGCCCTCAACATCTACTTAATAAAGCTCCGCGTGAGAACTGCTGCTACAA 540  
Db 219 GAGTCTGAGCCCTCAACATCTACTTAATAAAGCTCCGCGTGAGAACTGCTGCTACAA 160  
Qy 541 TTTTATCCCATTTGTTGGTGTATCTGTTTGTGTGGACACAGGATTTATCTCA 600  
Db 159 TTTTATCCCATTTGTTGGTGTATCTGTTTGTGTGGACACAGGATTTATCTCA 100  
Qy 601 ACTCAGCAGAGTGCATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 660  
Db 99 ACTCAGCAGAGTGCATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 40  
Qy 661 CTGAACCCACATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 699  
Db 39 CTGAACCCACATCTCTTGAAGTATGAGAACCAACATCTCCATTACAAAT 1

RESULT 10  
US-07-869-933-10  
; Sequence 10, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 nucleotides  
; TYPE: nucleic acid

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STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NTHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1174 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 107..880
US-07-869-933-10

Query Match
Best Local Similarity 100.0%; Score 699; DB 1; Length 1174;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 120
DB 242 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 301
QY 121 CACAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 180
DB 362 GAAGACAGTGGAGAAATACAAATGTTCAGACCAACAAAGTTTAAATGAGAGTGAACCTGTGATC 421
QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 300
DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 481
QY 301 CAGCCCTCTTCTCAGGTGCTCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 360
DB 482 CAGCCCTCTTCTCAGGTGCTCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGGGATGTGTACAAAGTCAAT 420
DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGGGATGTGTACAAAGTCAAT 601
QY 421 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 480
DB 602 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 661
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAGCTCCGGTGGAGAGTACTGGCTACAA 540
DB 662 GAGTCTGAGCCCTCAACATTTACTGTAAATAGCTCCGGTGGAGAGTACTGGCTACAA 721
QY 541 TTTTATCCCAATTTGTTGGTGGTGAATCTGTTCTGTGACACAGGATTTATTTATCTCA 600
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DB 722 TTTTATCCCAATTTGTTGGTGGTGAATCTGTTGTGTCGACAGGATTTATTTATCTCA 781
QY 601 ACTCAGCAGCAGGTCAACATTTCTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 660
DB 782 ACTCAGCAGCAGGTCAACATTTCTTCTTGAAGATTAAGAGAACCCAGGAAAGGCTTCAGACTT 841
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699
DB 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 11
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinnet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)..(880)
US-09-103-663-10
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Query Match
Best Local Similarity 100.0%; Score 699; DB 3; Length 1174;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 120
DB 242 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGTTT 301
QY 121 CACAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 180
DB 302 CACAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTTGAAATGCCAAATTT 361
QY 181 GAAGACAGTGGAGAAATACAAATGTTCAGACCAACAAAGTTTAAATGAGAGTGAACCTGTGATC 240
DB 362 GAAGACAGTGGAGAAATACAAATGTTCAGACCAACAAAGTTTAAATGAGAGTGAACCTGTGATC 421
QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 300
DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 481
QY 301 CAGCCCTCTTCTCAGGTGCTCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 360
DB 482 CAGCCCTCTTCTCAGGTGCTCTCTCTTCAAGGCTCTCTGAGGCTCTGAGGCTGAGGCTG 541
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGGGATGTGTACAAAGTCAAT 420
DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTTGAGGAACTGGGATGTGTACAAAGTCAAT 601
QY 421 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 480
DB 602 GCCACAGTGAAGACAGTGGAACTCTACTGTACGGGAAAGTGGGAGCTGGAGCTAT 661
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QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGAGTCCGCTGAGAGTACTGGCTACAA 540  
Db 662 GAGTCTGAGCCCTCAACATTACTGTATAAAGAGTCCGCTGAGAGTACTGGCTACAA 721  
QY 541 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTCTGTTGGGACACAGGATTTATCTCA 600  
Db 722 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTCTGTTGGGACACAGGATTTATCTCA 781  
QY 601 ACTCAGCAGAGTCACTTCTCTTGAAGATTAAAGAGAACAGGAAAGGCTTCAGACTT 660  
Db 782 ACTCAGCAGAGTCACTTCTCTTGAAGATTAAAGAGAACAGGAAAGGCTTCAGACTT 841  
QY 661 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 699  
Db 842 CTGAACCCCATCTTAAGCCAAACCCCAAAACAACTGA 880

RESULT 12  
US-08-756-387B-1  
; Sequence 1, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1198 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 107..877  
US-08-756-387B-1

Query Match 100.0%; Score 699; DB 2; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 2.le-221;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCAGGATAGAAATTTAAAGAGAG 60  
Db 182 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCAGGATAGAAATTTAAAGAGAG 241  
QY 61 AATGTGACTCTTACATGTAATGAGAACAAATTTCTTGAAGTCCAGTCCACCAATGGTTC 120

Db 242 AATGTGACTCTTACATGTAATGAGAACAAATTTCTTGAAGTCCAGTCCACCAATGGTTC 301  
QY 121 CACAATGGCAGCCCTTTCAGAGAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180  
Db 302 CACAATGGCAGCCCTTTCAGAGAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 361  
QY 181 GAACACAGTGGAGAAATACAAATGTGAGACACAAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAACACAGTGGAGAAATACAAATGTGAGACACAAACAAAGTTAATGAGAGTGAACCTGTGTAC 421  
QY 241 CTGGAAGTCTTCACTGAGTGGCTGCTCTCTTCAGGCCCTCTGCTGAGGTGGTGTATGGAGGGC 300  
Db 422 CTGGAAGTCTTCACTGAGTGGCTGCTCTCTTCAGGCCCTCTGCTGAGGTGGTGTATGGAGGGC 481  
QY 301 CAGCCCTCTTCTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360  
Db 482 CAGCCCTCTTCTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 541  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACACACACATCTCCATTACAAAT 420  
Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAACACACACATCTCCATTACAAAT 601  
QY 421 GCCACAGTTGAAGACAGTGAACCTTACTTCTGACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
Db 602 GCCACAGTTGAAGACAGTGAACCTTACTTCTGACGGGCAAAAGTGTGGCAGCTGGACTAT 661  
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAGTACTGGCTACAA 540  
Db 662 GAGTCTGAGCCCTCAACATTACTGTATAAAGCTCCGCTGAGAGTACTGGCTACAA 721  
QY 541 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTCTGTTGGACACAGGATTTATCTCA 600  
Db 722 TTTTATATCCCATTTGTTGGTGGTGAATCTGTTTCTGTTGGACACAGGATTTATCTCA 781  
QY 601 ACTCAGCAGAGTCACTTCTCTTGAAGATTAAAGAACCCAGAAAGGCTTCAGACTT 660  
Db 782 ACTCAGCAGAGTCACTTCTCTTGAAGATTAAAGAACCCAGAAAGGCTTCAGACTT 841  
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RESULT 13  
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; Sequence 3, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: DI-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1198 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-756-387B-3

Query Match 100.0%; Score 699; DB 2; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-221;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CACATGCGAGCTTTAGAGAGACAAATTCAGTTTGAATATGTGAATGCCAAATTT 180
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US-09-285-873-1  
 ; Sequence 1, Application US/09285873  
 ; Patent No. 6309832  
 ; GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.  
 APPLICANT: Porter, James P.  
 APPLICANT: Rushlow, Keith E.  
 APPLICANT: Wasson, Donald L.  
 TITLE OF INVENTION: Method to Detect Ige  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ADDRESSEE: Heska Corporation  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/285,873  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/756,387.  
 FILING DATE: No. 6309832ember 26, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: DI-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1198 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 107..877  
 US-09-285-873-1

Query Match 100.0%; Score 699; DB 4; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-221;  
 Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 GAGTCTGAGCCCTCAACATTAATCTGTAATAAAGCTCCCGGTGAGAGTACTGGCTACAA 540  
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QY 601 ACTCAGCAGCAGTCACTTTCTTTGAAGATTAAAGAACCCAGGAAAGCTTCAGACTT 660  
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QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
DB 842 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 880

## RESULT 15

US-09-285-873-3/C  
; Sequence 3, Application US/09285873  
; Patent No. 6309632  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IgE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heskia Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,873  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387  
; FILING DATE: No. 6309832ember 26, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1198 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-285-873-3

Query Match

100.0%; Score 699; DB 4; Length 1198;

Best Local Similarity 100.0%; Pred. No. 2.1e-221;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 417 ACTCAGCAGCAGTCACTTTCTTTGAAGATTAAAGAACCCAGGAAAGGCTTCAGACTT 358  
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Job time : 62.7962 secs

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ALIGNMENTS

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; Sequence 7, Application US/09944277A  
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; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION NUMBER: US/09/944,277A  
; APPLICATION NUMBER: 30-Aug-2001  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	699	100.0	1198	17	US-10-775-169-141
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; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

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Best Local Similarity 100.0%; Pred. No. 6.5e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

US-09-944-277A-4

; Sequence 4, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

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;
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington, Verser, Ph.D.
; Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

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Query Match          100.0%; Score 699; DB 9; Length 774;
Best Local Similarity 100.0%; Pred. No. 7e-218;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATCGAATAGAAATATTTAAAGGAGAG 60
Db 76 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATCGAATAGAAATATTTAAAGGAGAG 135

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 195

QY 121 CACAATGGCAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
Db 196 CACAATGGCAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 255

QY 181 GAAGACAGTGGAGAAATACAAATGTGTCAGCACCACCAAGTTAATGAGTGAACCTGTGTAC 240
Db 256 GAAGACAGTGGAGAAATACAAATGTGTCAGCACCACCAAGTTAATGAGTGAACCTGTGTAC 315

QY 241 CTGGAAGTCTTCAGTGAAGTGGTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCT 300
Db 316 CTGGAAGTCTTCAGTGAAGTGGTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCT 375

QY 301 CAGCCCTCTTCTCCTCAGTGGCAGTGGTGGAGAACTGGGATGTGTAAGTGTGATCTAT 360
Db 376 CAGCCCTCTTCTCCTCAGTGGCAGTGGTGGAGAACTGGGATGTGTAAGTGTGATCTAT 435

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361 TATAAGAGTGGTGAAGCTCTCAAGTACTGGTATGAGAACACCAACATCTCCATTACAAAT 420  
Db TATAAGAGTGGTGAAGCTCTCAAGTACTGGTATGAGAACACCAACATCTCCATTACAAAT 495  
421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTATCGGGGAAAGTGGGAGCTTGGACTAT 480  
Db GCCACAGTTGAAGACAGTGGAACTTACTACTGTATCGGGGAAAGTGGGAGCTTGGACTAT 555  
481 GAGTCTCAGCCCTCAACATTTACTGTATTAATAAAGCTCCGGGTGAGAACTACTGGCTACAA 540  
Db GAGTCTCAGCCCTCAACATTTACTGTATTAATAAAGCTCCGGGTGAGAACTACTGGCTACAA 615  
541 TTTTATATCCATTTGGTGGTGAATCTCTTGGTGTGGTGTGGACACAGATTTATTTCTCA 600  
Db TTTTATATCCATTTGGTGGTGAATCTCTTGGTGTGGTGTGGACACAGATTTATTTCTCA 675  
601 ACTCAGCAGAGCTCAGATTTCTTGAAGATTAAGAGACCAAGGAAAGCTTTCAGACTT 660  
Db ACTCAGCAGAGCTCAGATTTCTTGAAGATTAAGAGACCAAGGAAAGCTTTCAGACTT 735  
661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
Db CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 774

RESULT 3  
US-09-944-277A-5/c  
; Sequence 5, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-944-277A-5

Query Match 100.0%; Score 699; DB 9; Length 774;  
Best Local Similarity 100.0%; Pred. No. 7e-218;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTCCTCAGAACCTTAAGGTCTCTTGAACCTCCATCGAATAGATAATTTAAAGGAGAG 60  
Db GTCCCTCAGAACCTTAAGGTCTCTTGAACCTCCATCGAATAGATAATTTAAAGGAGAG 640  
QY 61 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATPGGTTTC 120  
Db AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATPGGTTTC 580  
QY 121 CACAATGCGAGCTTTTCAAGAGACAAATTCAGTTTGAATATTTGTAATGCGCAAAATTT 180  
Db CACAATGCGAGCTTTTCAAGAGACAAATTCAGTTTGAATATTTGTAATGCGCAAAATTT 520  
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAAAGTTAATGAGAGTGAACCTGTGTAC 460  
QY 241 CTGGAAGTCTTTCAGTGACTGGCTGCTCTTCAAGCTCTGCTGAGGCTCTGCTGAGTGGTGTATGAGGGC 300  
Db CTGGAAGTCTTTCAGTGACTGGCTGCTCTTCAAGCTCTGCTGAGGCTCTGCTGAGTGGTGTATGAGGGC 400  
QY 301 CAGCCCTCTTCTCAGGTGCTGCTGGAGAACTGGGATGTGTACAAGTGTATCTAT 360  
Db CAGCCCTCTTCTCAGGTGCTGCTGGAGAACTGGGATGTGTACAAGTGTATCTAT 340  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
Db TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 280  
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTCGGGCAAGTGGCAGCTGGACTAT 480  
Db GCCACAGTTGAAGACAGTGGAACTTACTACTGTCGGGCAAGTGGCAGCTGGACTAT 220  
QY 481 GAGTCTGAGCCCTCAACATTTACTCTAATAAAGCTCCGCGTGAGAACTTCTGGTACAA 540  
Db GAGTCTGAGCCCTCAACATTTACTCTAATAAAGCTCCGCGTGAGAACTTCTGGTACAA 160  
QY 541 TTTTATATCCATTTGGTGGTGAATCTTGTGTGGACACAGGATTTATTTCTCA 600  
Db TTTTATATCCATTTGGTGGTGAATCTTGTGTGGACACAGGATTTATTTCTCA 100  
QY 601 ACTCAGCAGAGCTCAGATTTCTTGAAGATTAAGAGAACCCAGGAAAGCTTTCAGACTT 660  
Db ACTCAGCAGAGCTCAGATTTCTTGAAGATTAAGAGAACCCAGGAAAGCTTTCAGACTT 40  
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 699  
Db CTGAACCCACATCTTAAGCCAAACCCCAAAACAACTGA 1

RESULT 4  
US-09-944-277A-1  
; Sequence 1, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
;

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match
Best Local Similarity 100.0%; Score 699; DB 9; Length 1198;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGGAATAGAAATTTAAAGGAGAG 60
DB 182 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGGAATAGAAATTTAAAGGAGAG 241
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGTTTC 120
DB 242 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGTTTC 301
QY 121 CACATGGCAGCTTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180
DB 302 CACATGGCAGCTTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 361
QY 181 GAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGATGAACTGTGTAC 240
DB 362 GAAGCAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGATGAACTGTGTAC 421
QY 241 CTGGAAGTCTTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGGTGGTGGAGGGC 300
DB 422 CTGGAAGTCTTTCAGTACTGCTGCTCTTCAGGCTCTCTGAGGTGGTGGAGGGC 481
QY 301 CAGCCCTCTCTTCAGTGGCCATGTTGGAGGAACCTGGAGTGTGTAAGGTGATCTAT 360
DB 482 CAGCCCTCTCTTCAGTGGCCATGTTGGAGGAACCTGGAGTGTGTAAGGTGATCTAT 541
QY 361 TATAGGATGTGAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 420
DB 542 TATAGGATGTGAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 601
QY 421 GCCACAGTTGAAGACAGTGGACCTTACTGTGTACGGGCAAGGTGGGAGCTGGACTAT 480
DB 602 GCCACAGTTGAAGACAGTGGACCTTACTGTGTACGGGCAAGGTGGGAGCTGGACTAT 661
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATTAAGCTCCGGTGGAGTACTGGCTACAA 540
DB 662 GAGTCTGAGCCCTCAACATTTACTGTAATTAAGCTCCGGTGGAGTACTGGCTACAA 721
QY 541 TTTTATCCCATTTGGTGGTCTGTTCTGTGGACACAGGATTTATTTATCTCA 600

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DB 722 TTTTATCCCATTTGGTGGTGAATCTGTTGCTGTGGACACAGGATTTATTTATCTCA 781
QY 601 ACTCAGCAGCAGGTCACTTTCTTTGAAGATTTAGAGAACCAAGGCTTTCAGACTT 660
DB 782 ACTCAGCAGCAGGTCACTTTCTTTGAAGATTTAGAGAACCAAGGCTTTCAGACTT 841
QY 661 CTGAACCCACATCTTAAGCCAAACCCCAAACTGA 699
DB 842 CTGAACCCACATCTTAAGCCAAACCCCAAACTGA 880

RESULT 5
US-09-944-277A-3/C
; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

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Query Match
Best Local Similarity 100.0%; Score 699; DB 9; Length 1198;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGGAATAGAAATTTAAAGGAGAG 60
DB 1017 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCTGGAATAGAAATTTAAAGGAGAG 958
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGTTTC 120
DB 957 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTCCACCAATGTTTC 898
QY 121 CACATGGCAGCTTTTCAGAGAGACAAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180

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897 CACAATGGCAGCCTTTTTCAGAGAGACAAATTCAGATTGTAATGCAAAATTT 838  
181 GAAGACAGTGGGAATACAAATCTCAGACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC 240  
837 GAAGACAGTGGGAATACAAATCTCAGACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC 778  
241 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGC 300  
777 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGC 718  
301 CAGCCCTCTTCTCAGTGGCTGCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 360  
717 CAGCCCTCTTCTCAGTGGCTGCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 658  
361 TATAAGGATGGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 420  
657 TATAAGGATGGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 598  
421 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 480  
597 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 538  
481 GAGTCTGAGCCCTCTCAACATCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 540  
537 GAGTCTGAGCCCTCTCAACATCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 478  
541 TTTTATCCATTTGAGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 600  
477 TTTTATCCATTTGAGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 418  
601 ACTCAGACAGTGGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 660  
417 ACTCAGACAGTGGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 358  
661 CTGAACCCACATCTCTTAAGCCAAACCCCAAAACCAACTGA 699  
357 CTGAACCCACATCTCTTAAGCCAAACCCCAAAACCAACTGA 319

RESULT 6  
US-09-962-832-244  
; Sequence 244, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE OF INVENTION: Sets  
; FILE REFERENCE: 689290-74  
; CURRENT APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,077  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,280  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 244  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-962-832-244

Query Match 100.0%; Score 699; DB 9; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 9.4e-218;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60  
Db 182 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 241  
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 120  
Db 242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 301

Qy 121 CACAATGGCAGCCTTTTTCAGAGAGACAAATTCAGATTGTAATGCAAAATTT 180  
Db 302 CACAATGGCAGCCTTTTTCAGAGAGACAAATTCAGATTGTAATGCAAAATTT 361  
Qy 181 GAAGACAGTGGGAATACAAATCTCAGACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAAGACAGTGGGAATACAAATCTCAGACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC 421  
Qy 241 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGC 300  
Db 422 CTGGAAGTCTTTCAGTGAAGTGGCTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGC 481  
Qy 301 CAGCCCTCTTCTCAGTGGCTGCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 360  
Db 482 CAGCCCTCTTCTCAGTGGCTGCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 541  
Qy 361 TATAAGGATGGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 420  
Db 542 TATAAGGATGGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 601  
Qy 421 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 480  
Db 602 GCACAGTGAAGACAGTGAAGTCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 661  
Qy 481 GAGTCTGAGCCCTCTCAACATCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 540  
Db 662 GAGTCTGAGCCCTCTCAACATCTCTCAAGTACTGATATGAGAACCAACCAATCTCCATTAACAAT 721  
Qy 541 TTTTATCCATTTGAGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 600  
Db 722 TTTTATCCATTTGAGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 781  
Qy 601 ACTCAGACAGTGGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 660  
Db 782 ACTCAGACAGTGGTGGTGGTCTCTTTCAGGCTCTCTCTGAGTGGTGTGAGGGTGTATCTAT 841  
Qy 661 CTGAACCCACATCTCTTAAGCCAAACCCCAAAACCAACTGA 699  
Db 842 CTGAACCCACATCTCTTAAGCCAAACCCCAAAACCAACTGA 880

RESULT 7  
US-10-775-169-141  
; Sequence 141, Application US/10775169  
; Publication No. US20040175743A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dörner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
; FILE REFERENCE: AM101080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 141  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-169-141

Query Match 100.0%; Score 699; DB 17; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 9.4e-218;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60  
Db 182 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 241  
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAAGTCCACCAATGTTTC 120



QY 421 GCCACAGTTGAACAGAGTGAACCTACTACTGTACCGGCAAAAGTGTGGCAGCTGGACTAT 480  
DB 521 GCCACAGTTGAACAGAGTGAACCTACTACTGTACCGGCAAAAGTGTGGCAGCTGGACTAT 580  
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAAGTACTGGCTACAA 540  
DB 581 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAAGTACTGGCTACAA 640  
QY 541 TTTTATATCCATGTTGGTGGTGAATCTGTGTTGCTGTGTGACACAGAGTATTTATCTCA 600  
DB 641 TTTTATATCCATGTTGGTGGTGAATCTGTGTTGCTGTGTGACACAGAGTATTTATCTCA 700  
QY 601 ACTCAGCAGCAGCTGCATCTTCTTGAAGATTAGAGAACCAAGGAGCTTCAGACTT 660  
DB 701 ACCCAGCAGCAGCTGCATCTTCTTGAAGATTAGAGAACCAAGGAGCTTCAGACTT 760  
QY 661 CTGAACCCACATCCTTAAGCCAAACCCCAAAACCAACTGA 699  
DB 761 CTGAACCCACATCCTTAAGCCAAACCCCAAAACCAACTGA 799

RESULT 9  
US-09-809-715-1  
; Sequence 1, Application US/09809715  
; Publication No. US2003003502A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardetzky, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Kinnet, Jean-Pierre  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC  
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE  
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF  
; FILE REFERENCE: AL-8  
; CURRENT APPLICATION NUMBER: US/09/809,715  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,853  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(528)  
US-09-809-715-1

Query Match 75.5%; Score 528; DB 10; Length 528;  
Best Local Similarity 100.0%; Pred. No. 6.3e-162;  
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60  
DB 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
DB 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
QY 121 CACAATGTCAGCTTTTGAAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180  
DB 121 CACAATGTCAGCTTTTGAAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180  
QY 181 GAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
DB 181 GAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTCAGTGAAGTGTCTCTTCAGGCTCTCTGAGGCTGTGATGGAGGC 300  
DB 241 CTGGAAGTCTTCAGTGAAGTGTCTCTTCAGGCTCTCTGAGGCTGTGATGGAGGC 300

QY 301 CAGCCCTCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAGTGTATCTAT 360  
DB 301 CAGCCCTCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAGTGTATCTAT 360  
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATACAAAT 420  
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATACAAAT 420  
QY 421 GCCACAGTTGAACAGAGTGAACCTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480  
DB 421 GCCACAGTTGAACAGAGTGAACCTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAG 528  
DB 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCTCCGCGTGAGAAG 528

RESULT 10  
US-10-293-992-1  
; Sequence 1, Application US/10293992  
; Publication No. US20040033527A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardetzky, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Kinnet, Jean-Pierre  
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR  
; TITLE OF INVENTION: CHAIN  
; FILE REFERENCE: AL-3-C1-1  
; CURRENT APPLICATION NUMBER: US/10/293,992  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/434,193  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,219  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 528  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(528)  
; OTHER INFORMATION:  
US-10-293-992-1

Query Match 75.5%; Score 528; DB 13; Length 528;  
Best Local Similarity 100.0%; Pred. No. 6.3e-162;  
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60  
DB 1 GTCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
DB 61 AATGTGACTCTTACATGTAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
QY 121 CACAATGTCAGCTTTTGAAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180  
DB 121 CACAATGTCAGCTTTTGAAGAGACAAATTCAGATTTGAATTTGAATGCCAAATTT 180  
QY 181 GAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
DB 181 GAAGACAGTGGAGAAATCAAAATGTGAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTCAGTGAAGTGTCTCTTCAGGCTCTCTGAGGCTGTGATGGAGGC 300  
DB 241 CTGGAAGTCTTCAGTGAAGTGTCTCTTCAGGCTCTCTGAGGCTGTGATGGAGGC 300  
QY 301 CAGCCCTCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAGTGTATCTAT 360  
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Db 301 CAGCCCTCTTCTCAGGTGGATGGTGGAGGAACTGGGATGTGTCAAGGTGATCTAT 360  
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Qy 421 GCCACAGTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 480  
 Db 421 GCCACAGTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 480  
 Qy 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCTCCGCGTGAGAAG 528  
 Db 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCTCCGCGTGAGAAG 528

## RESULT 11

US-09-944-277A-12

; Sequence 12, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; City: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: &lt;unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 516 nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..516

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-944-277A-12

Query Match 73.8%; Score 516; DB 9; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-158;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60  
 Db 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60

Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
 Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
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 Db 121 CACAATGGCAGGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180  
 Qy 181 GAAGACAGTGGAGATACAAATGTGAGCCAAACCAAGTTTAATGAGAGTGAACCTGTGTAC 240  
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 Db 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGGATGTGTACAAGTGATCTAT 360  
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGACGGGCAAGTGTGGCAGCTGGACTAT 480  
 Db 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGACGGGCAAGTGTGGCAGCTGGACTAT 480  
 Qy 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCT 516  
 Db 481 GAGTCTGAGCCCTCAACATTACTCTAATAAAGCT 516

## RESULT 12

US-10-293-992-3

; Sequence 3, Application US/10293992

; Publication No. US20040033527A1

; GENERAL INFORMATION:

; APPLICANT: Jardtzy, Theodore S.

; APPLICANT: Garman, Scott Clayton

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR

; TITLE OF INVENTION: CHAIN

; FILE REFERENCE: AL-3-Cl-1

; CURRENT APPLICATION NUMBER: US/10/293,992

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/434,193

; PRIOR FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/107,219

; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 3

; LENGTH: 516

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(516)

; OTHER INFORMATION:

US-10-293-992-3

Query Match 73.8%; Score 516; DB 13; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-158;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60  
 Db 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAG 60  
 Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120





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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(528)
US-09-809-715-3

Query Match      73.7%; Score 515.2; DB 10; Length 528;
Best Local Similarity 98.5%; Pred. No. 1e-157;
Matches 520; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCCTCTGACCCCTCCATGGAATGAATATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAACCTTAAGGTCCTCTGACCCCTCCATGGAATGAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCACCAAAATGGTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCACCAAAATGGTTC 120

QY 121 CACATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180
Db 121 CACATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180

QY 181 GAAGACAGTGGAGAAATACAAATTCAGTTCAGCAACCAACAGTTTAAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGAAATACAAATTCAGTTCAGCAACCAACAGTTTAAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTCAGTGAAGTCTGCTCTTCCAGGCCCTCTGCTGAGGTGGTGTGAGAGGC 300
Db 241 CTGGAAGTCTTCAGTGAAGTCTGCTCTTCCAGGCCCTCTGCTGAGGTGGTGTGAGAGGC 300

QY 301 CAGCCCTCTTCTCAGTGGCAGTGGTGGAGGAACCTGGAGTGTACAAAGTGTATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGGCAGTGGTGGAGGAACCTGGAGTGTACAAAGTGTATCTAT 360

QY 361 TATAAGGATGTGAAGTCTTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db 361 TATAAGGATGTGAAGTCTTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
Db 421 GCCACAGTGTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGGGTGAGAG 528
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGGGTGAGAG 528

RESULT 15
US-10-236-392-29
; Sequence 29, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Pasturajan, Meera
```

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; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shency, Suresh
; APPLICANT: Shinkets, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 29
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(680)
US-10-236-392-29

Query Match      65.1%; Score 455; DB 13; Length 757;
Best Local Similarity 83.3%; Pred. No. 7e-138;
Matches 582; Conservative 0; Mismatches 0; Indels 117; Gaps 1;

QY 1 GTCCCTCAGAACCTTAAGGTCCTCTGAAACCCCTCCATGGAATGAATATTTAAAGGAGAG 60
Db 101 GTCCCTCAGAACCTTAAGGTCCTCTGAAACCCCTCCATGGAATGAATATTTAAAGGAGAG 160

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCACCAAAATGGTTC 120
Db 161 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAAGTCAGTTCACCAAAATGGTTC 220

QY 121 CACATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 180
Db 221 CACATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAAATGCCAAATTT 280

QY 181 GAAGACAGTGGAGAAATACAAATTCAGTTCAGCAACCAACAGTTTAAATGAGAGTGAACCTGTGTAC 240
Db 281 GAAGACAGTGGAGAAATACAAATTCAGTTCAGCAACCAACAGTTTAAATGAGAGTGAACCTGTGTAC 301

QY 241 CTGGAAGTCTTCAGTGAAGTCTGCTCTTCCAGGCCCTCTGCTGAGGTGGTGTGAGAGGC 300
Db 302 CTGGAAGTCTTCAGTGAAGTCTGCTCTTCCAGGCCCTCTGCTGAGGTGGTGTGAGAGGC 301

QY 301 CAGCCCTCTTCTCAGTGGCAGTGGTGGAGGAACCTGGAGTGTACAAAGTGTATCTAT 360
Db 302 TGCATGGTTGGAGGAACCTGGAGTGTGTACAAAGTGTATCTAT 343

QY 361 TATAAGGATGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
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601	Qy	ACTCAGCAGCAGGTCAACATTTCTCTTGAAGATTTAAGAGAACCCAGGAAGCTTTCAGACTT	660
584	Db	ACTCAGCAGCAGGTCAACATTTCTCTTGAAGATTTAAGAGAACCCAGGAAGCTTTCAGACTT	643
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estov.\*
- 5: em\_estpl.\*
- 6: em\_estro.\*
- 7: em\_estro.\*
- 8: em\_estro.\*
- 9: gb\_estl.\*
- 10: gb\_estl.\*
- 11: gb\_estl.\*
- 12: gb\_estl.\*
- 13: gb\_estl.\*
- 14: gb\_estl.\*
- 15: em\_estfun.\*
- 16: em\_eston.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vrt.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vrl.\*
- 28: gb\_gssl.\*
- 29: gb\_gssl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	559.4	80.0	760	12	BG542157
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C	5	475.4	68.0	768	13	BQ573778
C	6	436.6	62.5	846	10	BF678252
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C	8	411.6	58.9	712	14	CA419024
C	9	367.6	52.6	669	10	AW612525
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C	12	308.4	44.1	488	13	EX110472
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C	19	212.6	30.4	394	10	AW357271
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C	21	184	26.3	478	12	BQ005218
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C	24	175.8	25.2	403	14	CB768694
C	25	173	24.7	446	9	AI676097
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C	28	168.6	24.1	1201	9	AL531122
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C	36	160.4	22.9	852	12	BI821954
C	37	156.6	22.4	528	14	CB152997
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C	40	154.4	22.1	1201	9	AL558081
C	41	151.4	21.7	344	12	BI341697
C	42	150.6	21.5	429	13	BY228345
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EST.  
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ORGANISM  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLC1523 row: h column: 14  
High quality sequence stop: 667.

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BM991911	UI-H-DF1-
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BF603113	268539 MA
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AL549464	AL549464
AL531122	AL531122
CD244068	AGENCOURT
BX399366	BX399366
AL514096	AL514096
BI768140	603056571
EX402696	EX402696
CB555672	MNSF0057-
EX45202	EX45202
BI821954	603039767
CB152997	K-EST0210
CD693938	EST10461
AUI37840	AUI37840
AL558081	AL558081
BI341697	369218 MA
BY228345	BY228345
BM364531	BS3200020
AW357272	40241 MAR
EX378677	EX378677

FEATURES  
source

## Location/Qualifiers

1. .810  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGAGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 88.1%; Score 615.8; DB 12; Length 810;  
Best Local Similarity 96.7%; Pred. No. 2.1e-171;  
Matches 672; Conservative 0; Mismatches 17; Indels 6; Gaps 4;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATCGAATAGATAATTTAAAGGAGAG 60  
DB 106 GTCCTCAGAACCTTAAGTCTCTTGAACCTCCATCGAATAGATAATTTAAAGGAGAG 165  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
DB 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 225  
QY 121 CACATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGTCGACCAATTT 180  
DB 226 CACATGGCAGCCTTTCAGAGAGACAATTTCAAGTTTGAATATTTGAATGTCGACCAATTT 285  
QY 181 GAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAGATGAACCTGTGTAC 240  
DB 286 GAAGACAGTGGAGATACAAATGTGACACCAACAAGTTAATGAGATGAACCTGTGTAC 345  
QY 241 CTGGAAGTCTTCAGTGAATGCTGCTCTTCAAGGCTCTGCTGAGGTTGATGGAGGC 300  
DB 346 CTGGAAGTCTTCAGTGAATGCTGCTCTTCAAGGCTCTGCTGAGGTTGATGGAGGC 405  
QY 301 CAGCCCTCTTCTCCTCAGTGCATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
DB 406 CAGCCCTCTTCTCCTCAGTGCATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 465  
QY 361 TATAAGGATGGTGAAGTCTTCAAGTACTGTGTATGAGAACCAACATCTCCATTTACAAAT 420  
DB 466 TATAAGGATGGTGAAGTCTTCAAGTACTGTGTATGAGAACCAACATCTCCATTTACAAAT 525  
QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTAT 480  
DB 526 GCCACAGTTGAAGCAGTGGAACTTACTGTACGGGCAAGTGTGCGAGCTGGACTAT 585  
QY 481 GAGCTGAGCCCTCAACATTTACTGTATATAAAGCTCCGGGTGAGAGAGTACTGGCTACAA 540  
DB 586 GAGCTGAGCCCTCAACATTTACTGT-ATAAAGCTCCGGGTGAGAGAGTACTGGCTACCA 644  
QY 541 TTTTATATCCATTTGTTGGTGTGATCTGTTTCTGTGGACAC--AGGATTTATCT 598  
DB 645 ATTTTATATCCATTTGTTGGTGTGATCTGTTTCTGTGGACAC--AGGATTTATCT 704  
QY 599 -CAACTCAGCAGCAGGTACATTTCTC--TTGAAGATTAAGAGAACCAAGGAGGCTTCA 655  
DB 705 CCAACTCAGCAGCAGGTACATTTCTCCTTTGACGATTAGAGAACCCGGAAGGGCTCA 764  
QY 656 GACTTCTGAACCCACATCTTAAGCCAAACCCAAA 690  
DB 765 GACTTCTGAACCCAAATTCCTTAAGCAAAACCCAAA 799

RESULT 2  
LOCUS

DEFINITION BG542157 760 bp mRNA linear EST 03-APR-2001  
602571381F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4695476 5',  
mRNA sequence.

## ACCESSION

VERSION BG542157

## KEYWORDS

SOURCE EST.

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 760)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov

## REFERENCE

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1521 row: b column: 21

High quality sequence stop: 751.

## FEATURES

Location/Qualifiers  
1. .760  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4695476"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGAGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 80.0%; Score 559.4; DB 12; Length 760;

Best Local Similarity 98.5%; Pred. No. 1.2e-154;

Matches 596; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

QY 92 TCTTTGAAGTCTCAGTTCACCAATGCTTCCAAATGGCAGCCTTTCAAGAGACAAAT 151  
DB 98 TGTAGAGTCTAGTTCACCAATGCTTCCAAATGGCAGCCTTTCAAGAGACAAAT 157  
QY 152 CAAGTTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACC 211  
DB 158 CAAGTTTGAATTTGTGAATGCCAAATTTGAAGACAGTGGAGATACAAATGTGACACC 217  
QY 212 AACAGTTAATGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTACGCTGCTCCCTTC 271  
DB 218 AACAGTTAATGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTACGCTGCTCCCTTC 277  
QY 272 AGGCTCTGCTGAGTGTGTGAGGCGCCAGCCCTCTTCTCAGGTGCCATGCTTGA 331  
DB 278 AGGCTCTGCTGAGTGTGTGAGGCGCCAGCCCTCTTCTCAGGTGCCATGCTTGA 337  
QY 332 GGAATCTGGATGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGT 391  
DB 338 GGAATCTGGATGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGT 397  
QY 392 ATGAGAACCAACATCTCCATTTACAAATGCCAGTGTGAAGACAGTGGAACTACTACT 451

Db 398 ATGAGAACCAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACT 457  
 QY 452 GTACGGCAAGAGTGTGGCAGCTGATATGAGTCTGAGCCCTCAACATTACTGTATTA 511  
 Db 458 GTACGGCAAGAGTGTGGCAGCTGATATGAGTCTGAGCCCTCAACATTACTGTATTA 517  
 QY 512 AAGCTCCGCTGAGAGTACTGGCTACAAATTTTATCCCAATGTTGGTGGTGAATCTGT 571  
 Db 518 AAGCTCCGCTGAGAGTACTGGCTACAAATTTTATCCCAATGTTGGTGGTGAATCTGT 576  
 QY 572 TTGCTGTGGACACAGGATTTATCTCACTCAGCAGGAGGTACATTTCTTTGAAGA 631  
 Db 577 TTGCTGTGGACACAGGATTTATCTCACTCAGCAGGAGGTACATTTCTTTGAAGA 636  
 QY 632 TTAAGAGAACCAAGAAA-GCCTTCAGACTTCTGAACCCACATCCTTAAGCCAAACCCAAA 690  
 Db 637 TTAAGAGAACCAAGAAAGGCTTCAGACTTCTGAACCCA-ATCCTTAAGCCAAACCCAAA 695  
 QY 691 AACAA 695  
 Db 696 AAAAA 700

RESULT 3  
 LOCUS BF679057  
 DEFINITION 602153315F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4294467 5',  
 mRNA sequence.

ACCESSION BF679057  
 VERSION 1  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 834)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.

EMAIL: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLCM1143 row: n column: 04  
 High quality sequence stop: 621.

Location/Qualifiers  
 1..834

## FEATURES

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4294467"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH\_MGC\_83"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgctctggcg); Site 2: SfiI  
 (ggcattatggcg); 5' and 3' adaptors were used in cloning  
 as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGCC-3'  
 and 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.4  
 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA)."

## ORIGIN

Query Match 76.3%; Score 533; DB 10; Length 834;  
 Best Local Similarity 95.3%; Pred. No. 8.8e-147;

Matches 582; Conservative 0; Mismatches 25; Indels 4; Gaps 3;  
 QY 1 GTCCCTCAGAAACCTTAAGGTCTCCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 Db 106 GTCCCTCAGAAACCTTAAGGTCTCCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 165  
 QY 61 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
 Db 166 AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 225  
 QY 121 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTGAATGCCAAATTT 180  
 Db 226 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTGAATGCCAAATTT 285  
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 286 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAAAGTTAATGAGAGTGAACCTGTGTAC 345  
 QY 241 CTGGAAGTCTTCAGTGAAGTCTCCTTCAGGCTCTCTGAGGCTCTGCTGAGTGGTGTGATGGAGGC 300  
 Db 346 CTGGAAGTCTTCAGTGAAGTCTCCTTCAGGCTCTCTGAGGCTCTGCTGAGTGGTGTGATGGAGGC 405  
 QY 301 CAGCCCTCTCTCCTCAGGTGGCCATGGTTGGAGGAACTGGGATGTGTACAAGTGTATCTAT 360  
 Db 406 CAGCCCTCTCTCCTCAGGTGGCCATGGTTGGAGGAACTGGGATGTGTACAAGTGTATCTAT 465  
 QY 361 TATAAGGATGTGAAGTCTCCTCAGTGAAGTCTGATGAGAACCAACCAATCTCCATTACAAAT 420  
 Db 466 TATAAGGATGTGAAGTCTCCTCAGTGAAGTCTGATGAGAACCAACCAATCTCCATTACAAAT 524  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAGTGTGGCAGTGGAGTGTAT 480  
 Db 525 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGCAAGTGTGGCAGTGGAGTGTAT 584  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGTCCCGTGAAGAGTACTGGGTACAA 540  
 Db 585 GAGTCTGAG-CCCTCAACATTTACTGTATAAAAGTCCCGTGAAGAGTACTGGGTACAA 643  
 QY 541 TTTTATATCCCATTT--GTTGGTGGTGTCTCTGTTGCTGTGGACACAGGATTTATCT 598  
 Db 644 ATTTTATCCCAATGGTGGCGTGAATTTCTGTTGGCGTGGACACAGGCTTATTTATCC 703  
 QY 599 CAACTCAGCAG 609  
 Db 704 TCACTCAGCGG 714  
 RESULT 4  
 LOCUS BG548515  
 DEFINITION 602576508F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4704624 5',  
 mRNA sequence.

ACCESSION BG548515  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 840)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.

EMAIL: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

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High quality sequence stop: 590.
FEATURES
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    1..840
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:4704624"
      /lab_host="DH10B (T1 phage-resistant)"
      /clone_lib="NIH_MGC_77"
      /note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site 1:
      3' adaptors were used in cloning as follows: 5' adaptor
      sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
      5'-ATCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A,
      C, or G and N = A, C, G, or T). Average insert size 1.9
      kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
      by PCR. This library was enriched for full-length clones
      and was constructed by Clontech Laboratories (Palo Alto,
      CA). Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      68.8%; Score 480.6; DB 12; Length 840;
  Best Local Similarity 87.1%; Pred. No. 3.3e-131;
  Matches 626; Conservative 0; Mismatches 69; Indels 24; Gaps 8;

QY 1 GTCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60
   |||||
Db 106 GTCCTCAGAAACCTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 165

QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGTTTC 120
   |||||
Db 166 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGTTTC 225

QY 121 CACAATGCGAGCTTTACAGAGAGACAATTCAGTTTGAATATTGTAATGCCAATTT 180
   |||||
Db 226 CACAATGCGAGCTTTACAGAGAGACAATTCAGTTTGAATATTGTAATGCCAATTT 285

QY 181 GAAGACAGTGAGAGATACAAATGTGACACCAACAAGTTAATAGAGTGAACCTGTGTAC 240
   |||||
Db 286 GAAGACAGTGAGAGATACAAATGTGACACCAACAAGTTAATAGAGTGAACCTGTGTAC 345

QY 241 CTGGAAGTCTTCAGTGACTGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGATGGAGGC 300
   |||||
Db 346 CTGGAAGTCTTCAGTGACTGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGATGGAGGC 405

QY 301 CAGCCCTCTTCTCAGTGCCATGGTGTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360
   |||||
Db 406 CAGCCCTCTTCTCAGTGCCATGGTGTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 465

QY 361 TATAGAGTGTGAGAGCTCTCAAGTACTGTGTATGAGAACACAAATCTCCATTAACAAT 420
   |||||
Db 466 TATAGAGTGTGAGAGCTCTCAAGTACTGTGTATGAGAACACAAATCTCCATTAACAAT 525

QY 421 --GCCACAGTTTGAAGACAGTGGAACTTAC-TACTGTACGGCAAGTGGCAGCTGGAC 477
   |||||
Db 526 TGCCACAGTTTGAAGACAGTGGAACTTAC-TACTGTACGGCAAGTGGCAGCTGGAC 585

QY 478 -----TATGAGTGTAGCCCTCAACATTTACTGTAA-----TAAAGCTCCGGT-- 522
   |||||
Db 586 CTATGAGTGTAGCCCTCAACATTTACTGTAA-----TAAAGCTCCGGTGA 645

QY 523 -GAGAAGTACTGGCTACAAATTTTATCCCATTTGTTGGTGTGATT--CTGTTTGTGTTG 579
   |||||
Db 646 AGAAGTACTTGGCTACAAATTTTATCCCATTTGTTGGTGTGATT--CTGTTTGTGTTG 705

QY 580 GACACAGGA-TTATTTATCTCAACTCAGCA--GCAGGTCAATTTCTTTGAAGATTAAAG 636
   |||||
Db 706 CACCCCGAATTATTTATCTCAACTCAGCA--GCAGGTCAATTTCTTTGAAGATTAAAG 765

QY 637 AGRACAGGAAGCTTCAGACTTCTGACCCACATCTTAAGCCAAACCCCAACAA 695
   |||||
Db 766 GAAACCCAGGAAGCTTCAGACTTCTGACCCACATCTTAAGCCAAACCCCAACAA 824

```

RESULT 5  
BQ573778/c  
LOCUS  
DEFINITION  
UI-H-EZO-bav-1-04-0-UI.s1 NCI CGAP Chl Homo sapiens cDNA clone  
UI-H-EZO-bav-1-04-0-UI 3', mRNA sequence.  
ACCESSION  
BQ573778.1 GI:21477095  
VERSION  
BQ573778.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
1 (bases 1 to 768)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
Orthopaedics  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-41, >AT-rich#Low complexity (matched complement)  
93-129, >LINE2 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

Location/Qualifiers  
1..768  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-EZO-bav-1-04-0-UI"  
/tissue\_type="Chondrosarcoma Grade II"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP Chl"  
/note="Organ: Left Pelvis; Vector: pRT3-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP Chl is a cDNA library containing the following  
tissue(s): Chondrosarcoma Grade II. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pRT3-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
TGATCACCCT.  
TAG\_TISSUE=grade-2-chondrosarcoma  
TAG\_LIB=UI-H-EZO  
TAG\_SEQ=ATCTAATATG"

ORIGIN  
Query Match 68.0%; Score 475.4; DB 13; Length 768;  
Best Local Similarity 99.6%; Pred. No. 1.1e-123;  
Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 222 TGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTGACTGGCTGCTCTTCAGGCTCTGC 281  
|||||  
Db 768 TGAGAGTGAACCTGTGTACCTGGAGTCTTCAGTGACTGGCTGCTCTTCAGGCTCTGC 709  
|||||  
QY 282 TGAGTGTGTATGAGGCGCAGCCCTCTTCTCAGTGCCATGTTGGAGGACTCGGA 341  
|||||  
Db 708 TGAGTGTGTATGAGGCGCAGCCCTCTTCTCAGTGCCATGTTGGAGGACTCGGA 649  
|||||



from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 93-129, >LINE2 (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

## Location/Qualifiers

1..707  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-E10-avo-p-24-0-UI"  
 /tissue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP E10"  
 /note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)  
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 NCI CGAP E10 is a cDNA library containing the following  
 tissue(s): Chondrosarcoma. The library was constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into p7T3-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tag for this library is ACATTGCAC.  
 TAG\_TISSUE=chondrosarcoma  
 TAG\_LIB=UI-H-E10  
 TAG\_SEQ=ACATTGCAC"

## ORIGIN

Query Match 59.7%; Score 417; DB 14; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-112; Indels 0; Gaps 0;  
 Matches 417; Conservative 0; Mismatches 0

QY 283 GAGTGGTGTGAGGGGCGAGCCCTCTTCCTCAGGTGCCATGTTGGAGAACTGGGAT 342  
 DB 707 GAGTGGTGTGAGGGGCGAGCCCTCTTCCTCAGGTGCCATGTTGGAGAACTGGGAT 648

QY 343 GTGTACAGGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGATGATGAAACAC 402  
 DB 647 GTGTACAGGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGATGATGAAACAC 588

QY 403 AACATCTCCATTACAAATGCCACAGTTGACACAGTGAACCTACTGTACGGGCAAA 462  
 DB 587 AACATCTCCATTACAAATGCCACAGTTGACACAGTGAACCTACTGTACGGGCAAA 528

QY 463 GTGTGGCAGTGGACTATGATCTGAGCCCTCAACATTAATGTAATAAAGTCCCGGT 522  
 DB 527 GTGTGGCAGTGGACTATGATCTGAGCCCTCAACATTAATGTAATAAAGTCCCGGT 468

QY 523 GAGAGTACTGCTACATTTTATCCATGTTGTTGGTGGTCTGTTGCTGTGGAC 582  
 DB 467 GAGAGTACTGCTACATTTTATCCATGTTGTTGGTGGTCTGTTGCTGTGGAC 408

QY 583 ACAGATTATTATCTCAACTCAGCAGAGTCTCATTTCTCTTGAAGATTAAAGAAAC 642  
 DB 407 ACAGATTATTATCTCAACTCAGCAGAGTCTCATTTCTCTTGAAGATTAAAGAAAC 348

QY 643 AGGAAGGCTTCAGACTTCAGCCCATCTTAAGCCCAACCCCAAAACCACTGA 699  
 DB 347 AGGAAGGCTTCAGACTTCAGCCCATCTTAAGCCCAACCCCAAAACCACTGA 291

## RESULT 8

CA419024/c  
 LOCUS CA419024 712 bp mRNA linear EST 07-NOV-2002  
 DEFINITION UI-H-E21-bbj-e-19-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone  
 UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.  
 ACCESSION CA419024  
 VERSION CA419024.1 GI:24781675

## KEYWORDS

Homo sapiens (human)  
 Homo sapiens  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 712)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
 Orthopaedics

CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA  
 sequence: 1-42, >(TAAA)n#Simple\_repeat (matched complement)  
 94-130, >LINE2 (matched complement)  
 Seq primer: M13 FORWARD

## POLYA=Yes.

## Location/Qualifiers

1..712

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-H-E21-bbj-e-19-0-UI"

/tissue\_type="Chondrosarcoma Grade II"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP Ch2"

/note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)  
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 NCI CGAP Ch2 is a normalized cDNA library containing the  
 following tissue(s): Chondrosarcoma Grade II. The library  
 was constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into p7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 TCATCAGCT.  
 TAG\_TISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=UI-H-E21  
 TAG\_SEQ=ATCTAATATG"

## ORIGIN

Query Match 58.9%; Score 411.6; DB 14; Length 712;  
 Best Local Similarity 98.3%; Pred. No. 9.7e-111;  
 Matches 414; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 279 TGCTGAGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTG 338  
 DB 712 TGCTGAGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTG 653

QY 339 GGATGTGTACAGGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGTTAGAA 398  
 DB 652 GGATGTGTACAGGTGATCTATTATAGATGGTGAAGCTCTCAAGTACTGTTAGAA 593

QY 399 CCACAACTCTCCATTACAAATGCCACAGTGAAGACAGTGAACCTACTACTGTACGGG 458  
 DB 592 CCACAACTCTCCATTACAAATGCCACAGTGAAGACAGTGAACCTACTACTGTACGGG 533

QY 459 CAAAGTGTGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAGCTCC 518  
 DB 532 CAAAGTGTGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAGCTCC 473



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Qy 519 GCGTGAGAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTTCTGT 578
Db 472 GCGTGAGAGTACTGGCTACAAATTTTATCCCATGTTGGTGGTGAATCTGTTTCTGT 413
Qy 579 GGACACAGGATTTATTTCTCAACTCAGCAGCAGGTACATTTCTCTTGAAGATTAAAGAG 638
Db 412 GGACACAGGATTTATTTCTCAACTCAGCAGCAGGTACATTTCTCTTGAAGATTAAAGAG 353
Qy 639 AACACAGAAAGGTTTCAGATCTTGTGAACCCACATCTTAAGCCAAACCCCAAAACACTG 698
Db 352 AACACAGAAAGGTTTCAGATCTTGTGAACCCACATCTTAAGCCAAACCCCAAAACACTG 293
Qy 699 A 699
Db 292 A 292

RESULT 9
AW612525/c 669 bp mRNA linear EST 23-MAR-2000
LOCUS h03f07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2954053 3'
DEFINITION similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
ALPHA-SUBUNIT (HUMAN); mRNA sequence.
ACCESSION AW612525
VERSION AW612525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 438.
FEATURES
Location/Qualifiers
1..669
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2954053"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following RAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 132376-132391, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
ORIGIN
Query Match 52.6%; Score 367.6; DB 10; Length 669;
Best Local Similarity 97.2%; Pred. No. 1.1e-97;
Matches 384; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
Qy 306 CCTCTTCTCAGGTCGCCATGTTGAGCAACTGGGATGTGTACAGGTGATCTATTATAA 610

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Db 669 CCTCTTCTCAGGTCGCCATGTTGAGCAACTGGGATGTGTACAGGTGATCTATTATAA 610
Qy 366 GGATGGTGAAGTCTCTCAAGTACTGTTATGAGAACACACATCTCCATTACAAATGCCAC 425
Db 609 GGATGGTGAAGTCTCTCAAGTACTGTTATGAGAACACACATCTCCATTACATATGCCAC 550
Qy 426 AGTTCAAGACAGTGGAACTTACTGTACGGGGCAAAAGTGTGGCAGCTGGACTATGAGTC 485
Db 549 AGTTCAAGACAGTGGAACTTACTGTACGGGGCAAGTGTGGCAGCTGGAAATATGAGTC 490
Qy 486 TGAGCCCTTCAACATTTACTGTAAATAAAGTCCCGGTGAGAGTACTGGCTACAA-TTTT 544
Db 489 TGAGCCCTTCAACATTTACTGTAAATAAAGTCTCTGGTGAAGTACTGGCTACAAATTTT 430
Qy 545 TTATCCCATTTGTTGGTGGTATCTCTGTTGTCGACACAGGATTTATTTATCTCAACTC 604
Db 429 TTATCCCATTTGTTGGTGGTATCTCTGTTGTCGACACAGGATTTATTTATCTCAACTC 370
Qy 605 AGCAGCAGGTCACTTTCTTTGAAGATTAAGAACACAGGAAAGGCTTCAGACTCTGA 664
Db 369 AGCAGCAGGTCACTTTCTTTGAAGATTAAGAACACAGGAAAGGCTTCAGACTCTGA 310
Qy 665 ACCACATCTTAAGCCAAACCCCAAAACAACTGA 699
Db 309 ACCACATCTTAAGCCAAACCCCAAAACAACTGA 275

RESULT 10
BF677190 818 bp mRNA linear EST 21-DEC-2000
LOCUS 60208725F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251469 5',
DEFINITION mRNA sequence.
ACCESSION BF677190
VERSION BF677190
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 818)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1074 row: n column: 14
High quality sequence stop: 616.
FEATURES
Location/Qualifiers
1..818
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4251469"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 83"
/note="Organ: Prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccattatggcc); Site 2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGCGGCGCCGACATG-(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."

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SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 488)  
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radelof, U., Schneider, D. and Korn, B.  
 TITLE Human Unigeneset - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No.972)  
 http://www.rzpd.de/Clonecards/cgi-bin/showlib.pl.cgi/?response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

FEATURES  
 source  
 1..488  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGP998B235736 ; IMAGE:2314294"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Pr28"  
 /notes="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI CGAP Pr22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneIDs  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
 Query Match 44.1%; Score 308.4; DB 13; Length 488;  
 Best Local Similarity 99.7%; Pred. No. 3,7e-80;  
 Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 390 GTATGAGAACCAACATCTCCATTACAAATGCGACAGTGAACAGTGGACCTACTA 449  
 Db 1 GTATGAGAACCAACATCTCCATTACAAATGCGACAGTGAACAGTGGACCTACTA 60  
 Qy 450 CTGTACGGGCAAGTGGAGCTGGACTAGCTGAGCCCTCAACATTTACTGTAAT 509  
 Db 61 CTGTACGGGCAAGTGGAGCTGGACTAGCTGAGCCCTCAACATTTACTGTAAT 120  
 Qy 510 AAAAGCTCCGGTGGAGAGTACTGGCTACAAATTTTTATCCCATTTGTGGTGAATCT 569  
 Db 121 AAAAGCTCCGGTGGAGAGTACTGGCTACAAATTTTTATCCCATTTGTGGTGAATCT 180  
 Qy 570 GTTTGCTGTGACACAGATTTATTTCTCACTCAGCAGAGTCACTTCTTTGAA 629  
 Db 181 GTTTGCTGTGACACAGATTTATTTCTCACTCAGCAGAGTCACTTCTTTGAA 240  
 Qy 630 GATTAAAGAACCCAGGAAGGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCAA 689  
 Db 241 GATTAAAGAACCCAGGAAGGCTTCAGACTTCTGAACCCATCTTAAGCCAAACCCCAA 300  
 Qy 690 AAACAACCTGA 699  
 Db 301 AAACAACCTGA 310

RESULT 13  
 CF362072  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

1..660  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3P1G"  
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
 library made with RNA pooled from multiple tissues  
 including brain, liver, muscle, placenta/endometrium,  
 ovary, testes, and bone marrow."

ORIGIN

Query Match 42.3%; Score 296; DB 14; Length 660;  
 Best Local Similarity 71.6%; Pred. No. 2.1e-76;  
 Matches 408; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

Qy 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60  
 Db 91 GTATCCAGGAATCTCAGGTGCTTGTATCCCCCATGGAATCGAATATTTAGAGGAGAG 150  
 Qy 61 AATGTGACTCTTACATGTAAATCGGAACAATTTCTTTTGAAGTCAGTTCCACCAATGGTTC 120  
 Db 151 AATGTGACTCTCAGATGTATTGGGAACGATGCTTGAATAATACCCCAATTTGGACA 210  
 Qy 121 CACATGGCAGCTTTTCAGAGAGACAATTCAGTTGAATTTGTGAATGCCAAATTT 180  
 Db 211 CACAACAACAACTTTGGAAGTGAACCTTCGATTGGACCTTAAGNAGTCAAAACCT 270  
 Qy 181 GAAGACAGTGGAGAAATACAAATGTTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 271 GGGGACAGCGCAAAATACAGATGCCAAGCAAAAGACTTTACAATGAGTGAACCTGTGCAC 330  
 Qy 241 CTGGAAGTCTTCAGTACTGGCTGCTCTTCAGGCTCTGCTGAGTGGTGTAGGAGGC 300  
 Db 331 CTGAAGTCTCAGTACTGGCTGCTCTTCAGACCTCTGTCCTCCGCTGTGAGGAGGC 390  
 Qy 301 CAGCCCTCTTCTCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAAGTGTATCTAT 360  
 Db 391 CAGTCTTCTCTCTCATGTGTACGGCTGGAAGATCTCAATGTCTTATAAGTGTATCTAC 450  
 Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACACATCTCCATTACAAAT 420

CF362072 660 bp mRNA linear EST 25-AUG-2003  
 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.  
 CF362072  
 EST  
 CF362072.1 GI:34161364

Sus scrofa (pig)  
 Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 660)

Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J.,  
 Wiss, T.A., Nonnen, D.J., Wray, J.E. and Keale, J.W.

A second set of porcine ESTs from a pooled-tissue normalized  
 library

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim\_alt option. Vector identified with

cross\_match v0.990329.

Plate: SRG8018 row: L column: 4

Seq primer: GTAATACGACTCACTATAGGG.

Location/Qualifiers

Db 451 TACAGGATGGAAGCCCTCAGTACTGGTATGAGAACCAACCTCTCCATTACCNAT 510  
 QY 421 GCACAGTTGAAGACAGTGGAACCTACTACTGTGTACGGGCAAGTGTGGCAGCTGAGCTAT 480  
 Db 511 GCCAAAGAGAGACAGTGGCTCTTATTGGTGCAGGGGCATAAATTCAAAAAATACCAAAA 570  
 QY 481 GAGTCTGAGCCCTCAGATTACTCTAATAAAGCTCCGCGT-----GAGAG 528  
 Db 571 AACTCTACTACTCTCACCATTACCAACAAAGAGATTCCTTCAGTTCCTCGAATAT 630  
 QY 529 TACTGGCTACAAATTTTATCCCATTTG 558  
 Db 631 TACTGGCTACAGCTTCATATCCCATTTG 660

RESULT 14  
 A1676114/c  
 LOCUS  
 DEFINITION 570 bp mRNA linear EST 17-DEC-1999  
 wc05e12.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:2314318 3',  
 similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR  
 ALPHA-SUBUNIT (HUMAN);, mRNA sequence.

ACCESSION A1676114  
 VERSION A1676114.1 GI:4876594  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 570)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing Arrayed by: Greg Lennon, Ph.D.  
 Clone Distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 625 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

FEATURES  
 source

1..570  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2314318"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_libs="NCI CGAP Pr28"  
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI CGAP Pr22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones IDs  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 36.3%; Score 254; DB 9; Length 570;  
 Best Local Similarity 88.7%; Fred. No. 6e-64;  
 Matches 275; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 390 GTATGAGAACCAACATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACCTACTA 449  
 Db 570 GTATGAGATCGCATCTGTGCCATAGCGAATGCCAGGTGATAGACAGTAGGCCCTATTG 511  
 QY 450 CTGTACGGGCAAGAGTGTGGCAGCTGAGCTATGAGTCTGAGCCCCCTCAACATTACTGTAT 509  
 Db 510 CTGTGCGGCAAGAGTGTGGCAGCTGAGCTATGAGTCTGAGCCCCCTCAACATTACTGTAT 451  
 QY 510 AAAAGCTCGCGTGAGAGTACTGGCTACAATTTTTATCCCATTTGTTGGTGGTATCT 569  
 Db 450 AAAAGCTCGCGTGAGAGTACTGGCTACAATTTTTATCCCATTTGTTGGTGGTATCT 391  
 QY 570 GTTTGCTGTGGACACAGGATTTATCTCAACTCAGCAGCAGGTACACATTCTCTTGAA 629  
 Db 390 GTTTGCTGTGGACACAGGATTTATCTCACTCAGCAGCAGGTACACATTCTCTTGAA 331  
 QY 630 GATTAAGAAACAGGAAAGGTTTCTGAGCTTCTGAAACCCACATCTCTAGCCAAACCCCA 689  
 Db 330 GATTAAGAAACAGGAGAGGTTTCTGAGCTTCTGAAACCCACATCTCTAGCCAAACCCCA 271  
 QY 690 AAACACTCGA 699  
 Db 270 AAACACTCGA 261

RESULT 15

BY752906

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY752906 652 bp mRNA linear EST 17-DEC-2002  
 BY752906 RIKEN full-length enriched, adult inner ear Mus musculus  
 cDNA clone F930034C11 5', mRNA sequence.

BY752906  
 BY752906.1 GI:27184082  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 652)  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaide, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gotohori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,  
 Chothia, C., Corbani, D.E., Cousins, S., Dalla, E., Dragani, T.,  
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Korno, H., Nakamura, M.,  
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

JOURNAL

MEDLINE

PUBMED

COMMENT

12466851

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Fukuda, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
Adachi, J., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
Ito, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
Takeda, Y., Waki, K., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National  
Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose  
assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

## FEATURES

source

Location/Qualifiers

1. .652

/organism="Mus musculus"

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Best Local Similarity 70.3%; Pred. No. 5.8e-63;
Matches 365; Conservative 0; Mismatches 148; Indels 6; Gaps 2;

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QY 118 TTCCCAATGGCAGCCTTTCAGAGAGACAAATTCAGTTTGAATATTGGAATGCCAAA 177
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Job time : 2359.62 secs

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DB 579 TATGAATCTGACAAATTCAGAAATTCGTGTAGTAAAGCT 617

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 3: gb\_in.\*
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- 6: gb\_pat.\*
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- 8: gb\_pl.\*
- 9: gb\_pr.\*
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- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	591	100.0	591	6	AR175486	AR175486 Sequence
2	591	100.0	591	6	AX074293	AX074293 Sequence
3	591	100.0	591	6	AX074295	AX074295 Sequence
4	591	100.0	713	6	E07699	E07699 cDNA encodi
5	591	100.0	773	6	AR219964	AR219964 Sequence
6	591	100.0	774	6	AR175481	AR175481 Sequence
7	591	100.0	774	6	AR175482	AR175482 Sequence
8	591	100.0	1068	6	A21606	A21606 human FC ep
9	591	100.0	1068	6	BD264325	BD264325 Recombina
10	591	100.0	1068	6	AX026808	AX026808 Sequence
11	591	100.0	1081	9	HUMMCIAA	J03605 Human mast
12	591	100.0	1102	9	BC005912	BC005912 Homo sapi
13	591	100.0	1106	9	BC015195	BC015195 Homo sapi
14	591	100.0	1174	6	AR123794	AR123794 Sequence
15	591	100.0	1198	6	AR175479	AR175479 Sequence
16	591	100.0	1198	6	AR175480	AR175480 Sequence
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18	591	100.0	1198	6	AX074289	AX074289 Sequence
19	591	100.0	1198	6	AX101304	AX101304 Sequence
20	591	100.0	1198	6	AX335621	AX335621 Sequence
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26	591	100.0	2955	6	AR219962	AR219962 Sequence
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42	504.4	85.3	528	6	BD267591	BD267591 Crystalli
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DEFINITION	AR175486	Sequence 10 from patent US 6309832.				
ACCESSION	AR175486	GI:117916785				
VERSION	AR175486.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 591)					
AUTHORS	Frank, G.R., Porter, J.P., Rushlow, K.E. and Wasson, D.L.					
TITLE	Method to detect Ige					
JOURNAL	Parent: US 6309832-A 10 30-OCT-2001;					
FEATURES	Location/Qualifiers					

Pred. No. is the number of results predicted by chance to have a

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RESULT 3
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LOCUS AX074293 591 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 7 from Patent WO0104310.
ACCESSION AX074293
VERSION AX074293.1 GI:12710480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1
Weber, E.R., Wood, K.V. and Hall, M.P.
Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 7 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
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ACCESSION AX074293
VERSION AX074293.1 GI:12710482
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
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Weber, E.R., Wood, K.V. and Hall, M.P.
Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 9 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
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VERSION E07699.1 GI:2175833			
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1 (bases 1 to 713)			
Ra.T., Naito.Y. and Hirama.M.			
PRODUCTION OF SOLUBLE HUMAN FcEPSILONRIALPHA CHAIN			
TITLE Patent: JP 1994169776-A 1 21-JUN-1994;			
JOURNAL RA TOMOYASU, GREEN CROSS CORP.THE			
COMMENT OS Homo sapiens (human)			
PN JP 1994169776-A/1			
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ACCESSION AR219964			

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ACCESSION AR219964



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Query Match 100.0%; Score 591; DB 6; Length 1068;  
Best Local Similarity 100.0%; Pred. No. 3.7e-174; Mismatches 0; Indels 0; Gaps 0;  
Matches 591; Conservative 0;

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LOCUS  
DEFINITION Recombinant soluble Fc receptors.  
BD264325  
ACCESSION  
VERSION BD264325.1 GI:33074093  
KEYWORDS JP 2002531086-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1068)  
AUTHORS Sondermann, P., Huber, R. and Jakob, U.  
TITLE Recombinant soluble Fc receptors  
JOURNAL Patent: JP 2002531086-A 8 24-SEP-2002;  
MAX PLANCK GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV  
COMMENT OS Homo sapiens (human)  
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PD 24-SEP-2002  
PF 03-DEC-1999 JP 2000585398  
PR 03-DEC-1998 EP 98122969.3

Best Local Similarity 100.0%; Pred. No. 3.4e-174;  
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A21606  
ACCESSION  
VERSION A21606.1 GI:579605  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 1068)  
AUTHORS  
TITLE HYBRID Fc RECEPTOR MOLECULES  
JOURNAL Patent: WO 9106570-A 29 16-MAY-1991;  
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PI PETER SONDERRMANN, ROBERT HUBER, UWE JAKOB  
 PC C12N15/09, A61K35/00, A61K45/00, A61P19/02, A61P29/00, A61P31/18,  
 A61P35/00,  
 PC A61P37/02, A61P37/08, C07K14/735, C12N1/21, G01N33/53, G01N33/53//  
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 DEFINITION Sequence 14 from Patent EP1006183.  
 ACCESSION AX026808  
 VERSION AX026808.1 GI:10187941  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1

AUTHORS  
 TITLE Recombinant soluble fc receptors  
 JOURNAL Patent: EP 1006183-A 14 07-JUN-2000;  
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 Best Local Similarity 100.0%; Pred. No. 3.7e-174;  
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 Db 580 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 630

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 DEFINITION Human mast cell IgE receptor alpha-chain.  
 ACCESSION J03605  
 VERSION J03605.1 GI:187449  
 KEYWORDS immunoglobulin-like sequence; receptor.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1081)  
 AUTHORS Shimizu, A., Tepler, I., Benfey, P.N., Berenstein, E.H., Siraganian, R.P., and Leder, P.  
 TITLE Human and rat mast cell high-affinity immunoglobulin E receptors: characterization of putative alpha-chain gene products  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (6), 1907-1911 (1988)

MEDLINE PUBMED COMMENT	88158102 2964640 Original source text: Human mast cell line KUB12, cDNA to mRNA, clone PAS-h-IgER-110B. Computer-readable copy of sequence in [1] kindly provided by P.Leder, 08-FEB-1988	DEFINITION	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide, mRNA (cDNA clone MGC:14507 IMAGE:4294467), complete cds.
FEATURES source	Location/Qualifiers 1..1081 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" <35..1081 /product="mast cell IgE receptor alpha-chain mRNA" 35..808 /note="mast cell IgE receptor alpha-chain" /codon_start=1 /protein_id="AA336204.1" /db_xref="GI:307164" /translation="MAPAMESPTLLCVALLFPDGLVAPQPKVSLNPNWRIKFG ENVTLTNGNFRFVSSTKWFHSLSEETNSLNIYNAKFDSGEVKCQHQVNESE FVILEVSDMLLQASREVNEGQPLRCHGRNWDYKVIYKGEKALKYVNHEN ISITNATVDSGTYCTGKWQLDYSESEPLNITVIKAPREKYLQFIFLVLVILFAV DTGLFISTQQQVTFLLKIKRKGFRLLNHPKPNKN" Unreported.	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	BC005912.1 BC005912 MGC. Homo sapiens (human)
MRNA		REFERENCE	1 (bases 1 to 1102)
CDS		AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whitting, M., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakeley, R.C., Grimwood, J., Schmutz, J., Myers, R.M., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krawinski, M.I., Skalska, U., Small, M.A., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
ORIGIN	Query Match 100.0%; Score 591; DB 9; Length 1081; Best Local Similarity 100.0%; Pred. No. 3.7e-174; Mismatches 0; Indels 0; Gaps 0; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TITLE	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabps@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: (Dickson, Mark) mcd@pax1.stanford.edu Contact: M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
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BC005912 1102 bp mRNA linear PRI 03-OCT-2003

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    LOCUS
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    alpha polypeptide, mRNA (cdna clone MGC:14717 IMAGE:4251469),
    complete cds.
    BC015195
    ACCESSION

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VERSION BC015195.1 GI:15929529
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1106)
AUTHORS
    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
    Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
    Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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    Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
    Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smillius,D.E.,
    Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
    Generation and initial analysis of more than 15,000 full-length
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    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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    2 (bases 1 to 1106)
    Strausberg,R.
    Direct Submission
    Submitted (01-OCT-2001) National Institutes of Health, Mammalian
    Gene Collection (MGC), Cancer Genomics Office, National Cancer
    Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
    USA
    REMARK
    COMMENT
    NIH-MGC Project URL: http://mgc.nci.nih.gov
    Contact: MGC help desk
    Email: cgabs-remail.nih.gov
    Tissue Procurement: CLONTECH
    cDNA Library Preparation: CLONTECH Laboratories, Inc.
    DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    Center, Stanford University School of Medicine, Stanford, CA 94305
    Web site: http://www-shgc.stanford.edu
    Contact: (Dickson, Mark) mcd@paxil.stanford.edu
    Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
    R. M.
    Clone distribution: MGC clone distribution information can be found
    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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DEFINITION Sequence 10 from patent US 6171803.  
ACCESSION AR123794  
VERSION AR123794.1 GI:14109155  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 1174)  
Kinet J.Pierre.  
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the high affinity receptor for immunoglobulin E  
Patent: US 6171803-A 10 09-JAN-2001;  
JOURNAL Location/Qualifiers  
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ACCESSION AR175479  
VERSION AR175479.1 GI:17916778  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1198)  
AUTHORS Frank, G.R., Porter, J.P., Rushlow, K.E. and Wassom, D.L.  
TITLE Method to detect IGE  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Sequence 4, Appl  
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ALIGNMENTS

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; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wasson, Donald E.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
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; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/494-9505  
; INFORMATION FOR SEQ ID NO: 10:  
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; TOPOLOGY: linear  
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; LOCATION: 1..591  
US-08-756-387B-10

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; Sequence 10, Application US/09285873
; Patent No. 6309832
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## GENERAL INFORMATION:

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; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Carol Talkington Verser, Ph.D.
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; ADDRESSEE: Heska Corporation
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; STREET: 1825 Sharp Point Drive
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; CITY: Fort Collins
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; STATE: Colorado
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; COUNTRY: USA
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; ZIP: 80525
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: Windows 95
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; SOFTWARE: WordPerfect for Windows, Version 7.0
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/285,873
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; FILING DATE:
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; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US/08/756,387
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; FILING DATE: No. 6309832ember 26, 1996
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; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
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; INFORMATION FOR SEQ ID NO: 10:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 591 nucleotides
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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; TOPOLOGY: linear
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; MOLECULE TYPE: cDNA
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; FEATURE:
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; NAME/KEY: CDS
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; LOCATION: 1..591
```

```
; US-09-285-873-10
```

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Query Match 100.0%; Score 591; DB 4; Length 591;
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Best Local Similarity 100.0%; Pred. No. 6.8e-186;
```

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Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGCTCCTGCCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCCTCGCTCA 60
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Db 1 ATGGCTCCTGCCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCCTCGCTCA 60
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QY 61 GATGGCGTGTAGCAGTCCCTCAGAACTCCTGAACTCCTGAACTCCATGGGAATAGA 120
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Db 61 GATGGCGTGTAGCAGTCCCTCAGAACTCCTGAACTCCTGAACTCCATGGGAATAGA 120
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QY 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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QY 181 TCCACCAATGTTTCCACATGGCAGCTTTCAGAGAGACAAATCAAGTTTGAATATT 240
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Db 181 TCCACCAATGTTTCCACATGGCAGCTTTCAGAGAGACAAATCAAGTTTGAATATT 240
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QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
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Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAG 300
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QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTGCTGCTCCTTCAGGCTCTGCTGAG 360
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Db 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTGCTGCTCCTTCAGGCTCTGCTGAG 360
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QY 361 GTGGTGTATGGAGGCGGAGCCCTCTTCCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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Db 361 GTGGTGTATGGAGGCGGAGCCCTCTTCCTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTG 420
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QY 421 TACAAGGTGATCTATTATTAAGGATGTGAAAGTCTCAAGTACTGTGTATGAGAACCAAC 480
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Db 421 TACAAGGTGATCTATTATTAAGGATGTGAAAGTCTCAAGTACTGTGTATGAGAACCAAC 480
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QY 481 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
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Db 481 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
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QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591
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Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591
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## RESULT 3

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US-09-944-277A-10
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; Sequence 10, Application US/09944277A
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; Patent No. 6682894
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; GENERAL INFORMATION:
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```
; APPLICANT: Frank, Glenn R.
```

```
; Porter, James P.
```

```
; Rushlow, Keith E.
```

```
; Wassom, Donald L.
```

;; TITLE OF INVENTION: Method to Detect Ige  
;; NUMBER OF SEQUENCES: 13  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Carol Talkington Verser, Ph.D.  
;; STREET: 1825 Sharp Point Drive  
;; CITY: Fort Collins  
;; STATE: Colorado  
;; COUNTRY: USA  
;; ZIP: 80525  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: Windows 95  
;; SOFTWARE: WordPerfect for Windows, Version 7.0  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 30-Aug-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/285,873  
;; FILING DATE: 1999-03-31  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Verser, Carol Talkington  
;; REGISTRATION NUMBER: 37,459  
;; REFERENCE/DOCKET NUMBER: DI-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 970/493-7272  
;; TELEFAX: 970/484-9505  
;; INFORMATION FOR SEQ ID NO: 10:  
;; SEQUENCE CHARACTERISTICS:  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cdna  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..591  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-944-277A-10  
Query Match 100.0%; Score 591; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 6,8e-186;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGTCCA 60  
DB 1 ATGGCTCTGTCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGTCCA 60  
QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCCTTGAACCCCTCATGAATAGA 120  
DB 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCCTTGAACCCCTCATGAATAGA 120  
QY 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAATCAGT 180  
DB 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAATCAGT 180  
QY 181 TCCACCAATGGTTCACCAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 240  
DB 181 TCCACCAATGGTTCACCAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 240  
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAG 300  
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAG 300  
QY 301 AGTGAACCTGTGTACTCTGAGTCTTTCAGTCACTGGCTGCTTTCAGGCTCTGCTGAG 360  
DB 301 AGTGAACCTGTGTACTCTGAGTCTTTCAGTCACTGGCTGCTTTCAGGCTCTGCTGAG 360  
QY 361 GTGGTGAATGGAGGCGACCCCTCTTCTCAGGTCCTGAGGAACTGGGATGTG 420  
DB 361 GTGGTGAATGGAGGCGACCCCTCTTCTCAGGTCCTGAGGAACTGGGATGTG 420

QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480  
DB 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480  
QY 481 ATCTCCATTACAAATGCCACAGTTGACAGACAGTGGAACTTACTGTACGGGCAAGTG 540  
DB 481 ATCTCCATTACAAATGCCACAGTTGACAGACAGTGGAACTTACTGTACGGGCAAGTG 540  
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591  
DB 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591

RESULT 4  
US-08-027-3  
; Sequence 3, Application US/08238027  
; Patent No. 5874404  
; GENERAL INFORMATION:  
; APPLICANT: RA, CHISEI  
; APPLICANT: NAITO, KOJI  
; APPLICANT: HIRAMA, MINORU  
; APPLICANT: OKUMURA, KO  
; TITLE OF INVENTION: ANTIALLERGIC COMPOSITION  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
; STREET: 2100 PENNSYLVANIA AVENUE  
; CITY: N.W.  
; STATE: WASHINGTON, D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20037-3202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/238,027  
; FILING DATE: 03-MAY-1994  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-229227  
; FILING DATE: 04-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-213002  
; FILING DATE: 10-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-270513  
; FILING DATE: 08-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-270514  
; FILING DATE: 08-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 4-270515  
; FILING DATE: 08-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-208217  
; FILING DATE: 29-JUL-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-197341  
; FILING DATE: 09-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-251605  
; FILING DATE: 07-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-251606  
; FILING DATE: 07-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-251608  
; FILING DATE: 07-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-261355

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; FILING DATE: 19-OCT-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-264802
; FILING DATE: 22-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-293-7060
; TELEFAX: 202-293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 120..713
; IDENTIFICATION METHOD: by similarity with known
; IDENTIFICATION METHOD: sequence or to an established consensus
US-08-238-027-3

Query Match 100.0%; Score 591; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 7.6e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCTTCGCTCCA 60
DB 120 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTTCTTCGCTCCA 179

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 180 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 239

QY 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 180
DB 240 ATATTAAAGGAGAGAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 299

QY 181 TCCACCAATGGTTCACCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 300 TCCACCAATGGTTCACCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 359

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCACCAAGTTAATGAG 300
DB 360 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCACCAAGTTAATGAG 419

QY 301 AGTGAACTGTGTACTGGAAGTCTTCAAGTGGCTGCTTCTTCAAGGCTCTGCTGAG 360
DB 420 AGTGAACTGTGTACTGGAAGTCTTCAAGTGGCTGCTTCTTCAAGGCTCTGCTGAG 479

QY 361 GTGGTGATGGAGGGGCGACCCCTTCTTCTCAGTGGCTGCTTGGAGGAACTGGGATGTG 420
DB 480 GTGGTGATGGAGGGGCGACCCCTTCTTCTCAGTGGCTGCTTGGAGGAACTGGGATGTG 539

QY 421 TACAAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480
DB 540 TACAAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 599

QY 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
DB 600 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 659

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
DB 660 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 710
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RESULT 5
US-08-997-956A-6
; Sequence 6, Application US/08997956A
; Patent No. 6423512
```

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; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

Query Match 100.0%; Score 591; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 8e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
DB 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120

QY 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 180
DB 121 ATATTAAAGGAGAGAATGTGACTCTTACATGTATGGAACAAATTTCTTTGAAGTCAGT 180

QY 181 TCCACCAATGGTTCACCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 181 TCCACCAATGGTTCACCAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCACCAAGTTAATGAG 300
DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCACCAAGTTAATGAG 300

QY 301 AGTGAACTGTGTACTGGAAGTCTTCAAGTGGCTGCTTCTTCAAGGCTCTGCTGAG 360
DB 301 AGTGAACTGTGTACTGGAAGTCTTCAAGTGGCTGCTTCTTCAAGGCTCTGCTGAG 360

QY 361 GTGGTGATGGAGGGGCGACCCCTTCTTCTCAGTGGCTGCTTGGAGGAACTGGGATGTG 420
DB 361 GTGGTGATGGAGGGGCGACCCCTTCTTCTCAGTGGCTGCTTGGAGGAACTGGGATGTG 420

QY 421 TACAAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480
DB 421 TACAAGGTGATCTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480

QY 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
DB 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
DB 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591
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RESULT 6
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
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421	"TCAAGGTGATCTATTATATGATGGTGAAGCTCTCAAGTACTCGGTATGAGAACCAAC	480
481	ATCTCATTTACAAATGCCACAGTTGAAGACAGTGGACCTACTACTACGGGCAAGTG	540
481	ATCTCATTTACAAATGCCACAGTTGAAGACAGTGGACCTACTACTACTCGGCAAGTG	540
541	TGCGACGTGGACTATGAGTCTGAGCCCTCAACTTCTGTAATAAAGCT	591
541	TGCGACGTGGACTATGAGTCTGAGCCCTCAACTTCTGTAATAAAGCT	591

## RESULT 7

US-08-756-387B-5/C  
 Sequence 5, Application US/08756387B  
 Patent No. 5945294  
 GENERAL INFORMATION:  
 APPLICANT: Frank, Glenn R.  
 APPLICANT: Porter, James P.  
 APPLICANT: Rushlow, Keith E.  
 APPLICANT: Wassom, Donald L.  
 TITLE OF INVENTION: Method to Detect IGE  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verwer, Ph.D.  
 ADDRESSEE: Heskia Corporation  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 5.0  
 CURRENT APPLICATION DATA: US/08756, 387B  
 APPLICATION NUMBER: US/08756, 387B  
 FILING DATE: No. 5945294ember 26, 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Verwer, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: DI-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 774 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-756-387B-5

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Query Match      100.0%; Score 591; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 8e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1	ATGGGTCGCGCATGGAAATCCCGTACTCTACTGTGTGTAGAGCTTACTGTTCITTCGGTCCA	60
774	ATGGGTCCTCGCATGGAAATCCCGTACTCTACTGTGTGTAGAGCTTACTGTTCITTCGGTCCA	715
61	GATGGGCGTGTAGCAGTCCCTCAGAAACCTAAAGGTCCTCTGAAACCGCTCATGGAATAGA	120
714	GATGGGCGTGTAGCAGTCCCTCAGAAACCTAAAGGTCCTCTGAAACCGCTCATGGAATAGA	655
121	ATATTTAAAGGAGAGATGTGACTCTTACATGTAAATGGGAACAAATTCITTTGAAGTCAGT	180
654	ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAAATTCITTTGAAGTCAGT	595
181	TCCACCAAAATGGTTCACAATGGCAGCCCTTTCAGAAGAGACAAATTCAGATTGAAATATT	240

APPLICANT: Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESSEE: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 774 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..774  
S-08-756-387B-4

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Query Match      100.0%; Score 591; DB 2; Length 774;
Best Local Similarity 100.0%; Pred. No. 8e-186;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1	ATGGCTCCTGCCATGGAAATCCCCTACTCTACTCTGTGTAGCCTTACTGTTCTTCGCTCCA	60
	QY	
1	ATGGCTCCTGCCATGGAAATCCCCTACTCTACTCTGTGTAGCCTTACTGTTCTTCGCTCCA	60
	DbB	
61	GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTCTGAAACCTCCATGGAAATAGA	120
	QY	
61	GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTCTGAAACCTCCATGGAAATAGA	120
	Db	
121	ATATTTAAAGGAGAGAAATGTGACTCTTCATGTAAATGGGAAACAAATTTCTTTGAAGTCAGT	180
	QY	
121	ATATTTAAAGGAGAGAAATGTGACTCTTCATGTAAATGGGAAACAAATTTCTTTGAAGTCAGT	180
	Db	
181	TCCACCAAAATGGTTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAGTTTCAATATT	240
	QY	
181	TCCACCAAAATGGTTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAGTTTCAATATT	240
	Db	
241	GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCAACAGTTTAATGAG	300
	QY	
241	GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTTCAGCACCAACAGTTTAATGAG	300
	Db	
301	AGTGAACCTGTGTACTTGGAAAGCTTTCAGTGACTGTGCTGCTCTTCAGGCCCTCTGCTGAG	360
	QY	
301	AGTGAACCTGTGTACTTGGAAAGCTTTCAGTGACTGTGCTGCTCTTCAGGCCCTCTGCTGAG	360
	Db	
361	GTGTGTGTGGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTTTGGAGGAACTGGGATGTG	420
	QY	
361	GTGTGTGTGGAGGGCCAGCCCTCTTCCTCAGGTGCCATGGTTTGGAGGAACTGGGATGTG	420
	Db	
421	TACAAAGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAAACCAAC	480
	QY	

Db 594 TCCACCAATGGTTCCCAATGGCAGCCTTTTCAGAGACAAATTCAGTTTGAATATT 535  
Qy 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAG 300  
Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAG 475  
Qy 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTCTTCAGGCTCTCTCTGAG 360  
Db 474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTCTTCAGGCTCTCTCTGAG 415  
Qy 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGTTGGAGGAAGTGGAGTGTG 420  
Db 414 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGTTGGAGGAAGTGGAGTGTG 355  
Qy 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAGTACTCTGTATGAGAACCAAC 480  
Db 354 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAGTACTCTGTATGAGAACCAAC 295  
Qy 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAGTG 540  
Db 294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAGTG 235  
Qy 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591  
Db 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 184

## RESULT 8

US-09-285-873-4  
; Sequence 4, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,873  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387  
; FILING DATE: No. 6309832ember 26, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: 1..774  
US-09-285-873-4  
Query Match  
Best Local Similarity 100.0%; Score 591; DB 4; Length 774;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTAGCTTACTGTCTTTCGTCTCA 60  
Db 1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTAGCTTACTGTCTTTCGTCTCA 60  
Qy 61 GATGGCTGTGTACAGTCCCTCAGAACTTAAAGTCTCTCTTGAACCCCTCCATGGAATAGA 120  
Db 61 GATGGCTGTGTACAGTCCCTCAGAACTTAAAGTCTCTCTTGAACCCCTCCATGGAATAGA 120  
Qy 121 ATATTTAAAGGAGAGAAATGTACTCTTACATGTAATGGAAACAATTTCTTTGAAGTCAGT 180  
Db 121 ATATTTAAAGGAGAGAAATGTACTCTTACATGTAATGGAAACAATTTCTTTGAAGTCAGT 180  
Qy 181 TCCACCAATGGTTCCCAATGGCAGCCTTTTCAGAGACAAATTCAGTTTGAATATT 240  
Db 181 TCCACCAATGGTTCCCAATGGCAGCCTTTTCAGAGACAAATTCAGTTTGAATATT 240  
Qy 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAG 300  
Db 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAG 300  
Qy 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTCTTCAGTGGAGAACTGGGATGTG 360  
Db 301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTCTCTCTTCAGTGGAGAACTGGGATGTG 360  
Qy 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGTTGGAGGAAGTGGGATGTG 420  
Db 361 GTGGTGAATGGAGGGCCAGCCCTCTTCCTCAGTGCCATGTTGGAGGAAGTGGGATGTG 420  
Qy 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480  
Db 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAAC 480  
Qy 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAGTG 540  
Db 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTCTACTGTACGGGCAAGTG 540  
Qy 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591  
Db 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591

## RESULT 9

US-09-285-873-5/c  
; Sequence 5, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0

Tue Oct 12 09:19:20 2004

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
;
; US-09-285-873-5
;
; Query Match 100.0%; Score 591; DB 4; Length 774;
; Best Local Similarity 100.0%; Pred. No. 8e-186;
; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ATGGCTCTGCGCATGGAATCCCTTACTGTGTGTAGCCTTACTGTTCCTTGGCTCCA 60
; DB 774 ATGGCTCTGCGCATGGAATCCCTTACTGTGTGTAGCCTTACTGTTCCTTGGCTCCA 715
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; QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
; DB 714 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 655
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; QY 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
; DB 654 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 595
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; QY 181 TCCACCAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGTTGAATATT 240
; DB 594 TCCACCAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGTTGAATATT 535
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; QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
; DB 534 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 475
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; QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTGCTGAG 360
; DB 474 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTGCTGAG 415
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; QY 361 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGTGCCATGTTGGAGAACTGGGATGTG 420
; DB 414 GTGGTGATGGAGGCGCAGCCCTCTTCTCAGTGCCATGTTGGAGAACTGGGATGTG 355
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; QY 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTCAAGTACTGGTATGAGAACCAAC 480
; DB 354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 295
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; QY 481 ATCTCCATACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGCAAGTG 540
; DB 294 ATCTCCATACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGCAAGTG 235
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; QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
; DB 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 184
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; RESULT 10
; US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
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;
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;
; US-09-944-277A-4
;
; Query Match 100.0%; Score 591; DB 4; Length 774;
; Best Local Similarity 100.0%; Pred. No. 8e-186;
; Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 ATGGCTCTGCGCATGGAATCCCTTACTGTGTGTAGCCTTACTGTTCCTTGGCTCCA 60
; DB 1 ATGGCTCTGCGCATGGAATCCCTTACTGTGTGTAGCCTTACTGTTCCTTGGCTCCA 60
;
; QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
; DB 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120
;
; QY 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
; DB 121 ATATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180
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; QY 181 TCCACCAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGTTGAATATT 240
; DB 181 TCCACCAATGGTTCACAAATGGCAGCCTTTCAGAGAGACAAATTCAGTTGAATATT 240
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; QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
; DB 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACCAAGTTAATAG 300
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; QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTGCTGAG 360
; DB 301 AGTGAACCTGTGTACCTGGAAGTCTTCAAGTCACTGGCTCTCTTCAAGGCTCTGCTGAG 360
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Qy 361 GTGGTGTAGAGGGCCAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTG 420  
 Db 361 GTGGTGTAGAGGGCCAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGGATGTG 420  
 Qy 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTAGAGAACCAAC 480  
 Db 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTAGAGAACCAAC 480  
 Qy 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 540  
 Db 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 540  
 Qy 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591  
 Db 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591

## RESULT 11

US-09-944-277A-5/c  
 ; Sequence 5, Application US/09944277A  
 ; Patent No. 6682894

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.  
 Porter, James P.  
 Rushlow, Keith E.  
 Wassom, Donald L.  
 TITLE OF INVENTION: Method to Detect Ige  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Carol Talkington Verser, Ph.D.  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-944-277A-5

Query Match

Best Local Similarity 100.0%; Score 591; DB 4; Length 774;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 60

Db 774 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTCGCTCCA 715

Qy 61 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120  
 Db 714 GATGGCGTGTAGCAGTCCCTCAGAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGA 655  
 Qy 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 180  
 Db 654 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGT 595  
 Qy 181 TCACCAAAATGGTTCCACANTGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 240  
 Db 594 TCACCAAAATGGTTCCACAAATGGCAGCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 535  
 Qy 241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAG 300  
 Db 534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTGAGCAACCAAGTTAATGAG 475  
 Qy 301 AGTGAACCTGTGTACCTGGAAATCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAG 360  
 Db 474 AGTGAACCTGTGTACCTGGAAATCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAG 415  
 Qy 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 420  
 Db 414 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 355  
 Qy 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTAGAGAACCAAC 480  
 Db 354 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGTGTAGAGAACCAAC 295  
 Qy 481 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 540  
 Db 294 ATCTCCATTACAATGCCACAGTTGAAGACAGTGGAACTTACTGTACTACGGGCAAGTG 235  
 Qy 541 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 591  
 Db 234 TGSCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATTAAGAGCT 184

## RESULT 12

US-07-869-933-10

; Sequence 10, Application US/07869933

; Patent No. 5770396

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933

FILING DATE: 19920416

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/154 NTHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 10:



SEQUENCE CHARACTERISTICS:  
LENGTH: 1174 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 107..880  
US-07-869-933-10

Query Match 100.0%; Score 591; DB 1; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 1e-185;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 60  
DB 107 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120  
DB 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 226

QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180  
DB 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

QY 181 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATATT 240  
DB 287 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 300  
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 360  
DB 407 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 420  
DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 526

QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAACAAC 480  
DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAACAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 540  
DB 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 646

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 697

RESULT 13  
US-09-103-663-10  
; Sequence 10, Application US/09103663D  
; Patent No. 6171803  
; GENERAL INFORMATION:  
; APPLICANT: Kinet et al.  
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta  
; TITLE OF INVENTION: subunit of the high affinity receptor for  
; TITLE OF INVENTION: immunoglobulin E.  
; FILE REFERENCE: 50490  
; CURRENT APPLICATION NUMBER: US/09/103,663D  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 07/869,933  
; EARLIER FILING DATE: 1992-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10

LENGTH: 1174  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (107)..(880)  
US-09-103-663-10

Query Match 100.0%; Score 591; DB 3; Length 1174;  
Best Local Similarity 100.0%; Pred. No. 1e-185;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 60  
DB 107 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 120  
DB 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGA 226

QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180  
DB 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

QY 181 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATATT 240  
DB 287 TCCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAAAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 300  
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGATACAAATCTCAGCACCAACCAAGTTAATGAG 406

QY 301 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 360  
DB 407 AGTGAACCTGTGTACCTGGAAGTCTTCACTGAGTGGCTGCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 420  
DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGTGGCCATGGTTGGAGGAACCTGGATGTG 526

QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAACAAC 480  
DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGTCTCTCAAGTACTGGTATGAGAACCAACAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 540  
DB 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 646

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 697

RESULT 14  
US-08-756-387B-1  
; Sequence 1, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wasom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: WordPerfect for Windows, Version 7.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/756,387B
/ FILING DATE: NO. 5945294ember 26, 1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Verser, Carol Talkington
/ REGISTRATION NUMBER: 37,459
/ REFERENCE/DOCKET NUMBER: DI-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 970/493-7272
/ TELEFAX: 970/484-9505
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1198 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 107..877
/
US-08-756-387B-1

Query Match 100.0%; Score 591; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 60
DB 107 ATGGCTCTGCGCATGGAATCCCTACTCTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 166

QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 226

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAGCAATTTCTTTGAAGTCAGT 180
DB 227 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAGCAATTTCTTTGAAGTCAGT 286

QY 181 TCACCAAAATGGTTCCAAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 240
DB 287 TCACCAAAATGGTTCCAAATGGCAGCCTTTTCAGAGAGACAAATTCAGTTTGAATATT 346

QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAAGTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAAGTTAATGAG 406

QY 301 AGTGAACCTGTGACTCTGGAAGTCTTCAAGTGTGCTGCTCTTTCAGGCTCTGCTGAG 360
DB 407 AGTGAACCTGTGACTCTGGAAGTCTTCAAGTGTGCTGCTCTTTCAGGCTCTGCTGAG 466

QY 361 GTGGTGTAGGAGGCGCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420
DB 467 GTGGTGTAGGAGGCGCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 526

QY 421 TACAGGTGTACTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGATGAGAACCAAC 480
DB 527 TACAGGTGTACTATTATTAAGATGGTGAAGCTCTCAAGTACTGATGATGAGAACCAAC 586

QY 481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 540
DB 587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTG 646

QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAATGTAATAAAGCT 591
DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAATGTAATAAAGCT 697

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US-08-756-387B-3/c
/ Sequence 3, Application US/08756387B
/ Patent No. 5945294
/ GENERAL INFORMATION:
/ APPLICANT: Frank, Glenn R.
/ APPLICANT: Porter, James P.
/ APPLICANT: Rushlow, Keith E.
/ APPLICANT: Wassom, Donald L.
/ TITLE OF INVENTION: Method to Detect Ige
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Carol Talkington Verser, Ph.D.
/ ADDRESSEE: Heskia Corporation
/ STREET: 1825 Sharp Point Drive
/ CITY: Fort Collins
/ STATE: Colorado
/ COUNTRY: USA
/ ZIP: 80525
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: Windows 95
/ SOFTWARE: WordPerfect for Windows, Version 7.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/756,387B
/ FILING DATE: NO. 5945294ember 26, 1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Verser, Carol Talkington
/ REGISTRATION NUMBER: 37,459
/ REFERENCE/DOCKET NUMBER: DI-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 970/493-7272
/ TELEFAX: 970/484-9505
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1198 nucleotides
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/
US-08-756-387B-3

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Best Local Similarity 100.0%; Pred. No. 1e-185;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1032 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 973

QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAGCAATTTCTTTGAAGTCAGT 180
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DB 852 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTACGACCAACAAAGTTAATGAG 793

QY 301 AGTGAACCTGTGACTCTGGAAGTCTTCAAGTGTGCTGCTCTTTCAGGCTCTGCTGAG 360
DB 792 AGTGAACCTGTGACTCTGGAAGTCTTCAAGTGTGCTGCTCTTTCAGGCTCTGCTGAG 733

QY 361 GTGGTGTAGGAGGCGCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420

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Qy	481	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG	540	
Db	612	ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG	553	
Qy	541	TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTATAAAGCT	591	
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:20:22 ; Search time 344.307 Seconds  
(without alignments)  
8701.874 Million cell updates/sec

Title: US-10-763-400-10

Perfect score: 591

Sequence: 1 atggcctgcgcgaatc.....acattactgtaataaaagct 591

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Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
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- 18: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	591	100.0	774	9	US-09-944-277A-4
3	591	100.0	774	9	US-09-944-277A-5
4	591	100.0	898	13	US-10-236-392-27
5	591	100.0	1198	9	US-09-944-277A-1
6	591	100.0	1198	9	US-09-944-277A-3
7	591	100.0	1198	9	US-09-962-832-244
8	591	100.0	1198	17	US-10-775-169-141
9	516	87.3	516	9	US-09-944-277A-12
10	516	87.3	516	13	US-10-293-992-3
11	516	87.3	528	10	US-09-809-715-1
12	516	87.3	528	13	US-10-293-992-1
13	516	87.3	699	9	US-09-944-277A-7
14	503.2	85.1	528	10	US-09-809-715-3

15	347	58.7	757	13	US-10-236-392-29
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21	298.6	50.5	708	16	US-10-434-817-6
22	298.6	50.5	708	16	US-10-434-817-8
23	168.6	28.5	2202	15	US-10-198-846-13731
24	167	28.3	765	15	US-10-027-736A-8
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ALIGNMENTS

RESULT 1

US-09-944-277A-10

; Sequence 10, Application US/09944277A

; Patent No. US00030034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

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; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 591 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..591
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match      100.0%; Score 591; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.6e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCTCTGCGCATGGAATCCCTCTACTCTACTGTGTAGCTTACTGTCTTCGCTCCA 60

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DB 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120

QY 121 ATATTAAAGGAGAGAAATGTACTCTTACATGTATGGAACAATTTCTTGAAGTCAGT 180
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QY 361 GTGGTGTAGAGGGGCGAGCCCTCTTCTCAGGTGCTTCAAGTGTCTTCAAGTGTCTTCAAGTGT 420
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QY 541 TGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTGTATAAAGCT 591
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## RESULT 2

US-09-944-277A-4  
 ; Sequence 4, Application US/09944277A  
 ; Patent No. US20020034771A1

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

Porter, James P.

Rushlow, Keith E.

Wasson, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

Heska Corporation

```

; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/484-9505
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 774 nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..774
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

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Query Match 100.0%; Score 591; DB 9; Length 774;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-183;  
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGCTCTGCGCATGGAATCCCTCTACTCTACTGTGTAGCTTACTGTCTTCGCTCCA 60

QY 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120
DB 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120

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QY 181 TCCACCAATAGTGTCCCAATGGCAGCCCTTTCAGAAAGAGACAAATTCAGTTTGAATATT 240
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## RESULT 3

US-09-944-277A-5/c  
; Sequence 5, Application US/09944277A  
; Patent No. US20020034771A1

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

Porter, James P.

Rushlow, Keith E.

Wassom, Donald L.

TITLE OF INVENTION: Method to Detect IGE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 774 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-944-277A-5

Query Match 100.0%; Score 591; DB 9; Length 774;  
Best Local Similarity 100.0%; Pred. No. 4.3e-183;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTCTGCTCCA 60  
DB 774 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTTCTGCTCCA 715  
QY 61 GATGGCGTTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120  
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QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTG 420  
DB 414 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTGGAGAACTGGGATGTG 355  
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DB 234 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTAATTAATAAAGCT 184

## RESULT 4

US-10-236-392-27

; Sequence 27, Application US/10236392

; Publication No. US20040067490A1

; GENERAL INFORMATION:

APPLICANT: Anderscn, David W

APPLICANT: Boldog, Ferenc L

APPLICANT: Burgess, Catherine, E

APPLICANT: Casman, Stacie J

APPLICANT: Catterton, Elina

APPLICANT: Chapoval, Andrei

APPLICANT: Crabtree, Julie

APPLICANT: Edinger, Shlomit, R

APPLICANT: Ellerman, Karen

APPLICANT: Gerlach, Valerie

APPLICANT: Gorman, Linda

APPLICANT: Grosse, William M

APPLICANT: Gusev, Vladamir

APPLICANT: Kekuda, Ramesh

APPLICANT: LaRochelelle, William J

APPLICANT: Li, Li

APPLICANT: MacDougall, John R

APPLICANT: Malyankar, Uriel M

APPLICANT: Miller, Charles E

APPLICANT: Millet, Isabelle

APPLICANT: Padigaru, Muralidhara

APPLICANT: Patturajan, Meera

APPLICANT: Pena, Carol A

APPLICANT: Peyman, John A

APPLICANT: Rastelli, Luca

APPLICANT: Reiger, Daniel K

APPLICANT: Rotherberg, Mark E

APPLICANT: Shenoy, Suresh

APPLICANT: Shinkets, Richard A

APPLICANT: Smithson, Glenda

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-442A

CURRENT APPLICATION NUMBER: US/10/236,392

CURRENT FILING DATE: 2002-09-06

PRIOR APPLICATION NUMBER: US09/540,763

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: US60/390,155

PRIOR FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US09/635,949

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; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 27
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(797)
US-10-236-392-27

Query Match      100.0%; Score 591; DB 13; Length 898;
Best Local Similarity 100.0%; Pred. No. 4.8e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTTCTTTCGCTCCA 60
DB 26 ATGGCTCTGCGATGGAATCCCTACTCTACTGTGTGTAGCTTACTTCTTTCGCTCCA 85
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCATGGAATAGA 120
DB 86 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTCTTGAACCCCTCCATGGAATAGA 145
QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 180
DB 146 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 205
QY 181 TCCACCAATGCTTCCCAATGCGAGCCTTTTACAGAGAGACAAATTTCAAGTTTGAATATT 240
DB 206 TCCACCAATGCTTCCCAATGCGAGCCTTTTACAGAGAGACAAATTTCAAGTTTGAATATT 265
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACGACCAACCAAGTTTAATGAG 300
DB 266 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACGACCAACCAAGTTTAATGAG 325
QY 301 AGTGAACCTGTACTGGAAGTCTTCAAGTACTGCTGCTTCTCAGGCTTCTGCTGAG 360
DB 326 AGTGAACCTGTACTGGAAGTCTTCAAGTACTGCTGCTTCTCAGGCTTCTGCTGAG 385
QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTCCTCATGGTGGAGAACTGGGATGTG 420
DB 386 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTCCTCATGGTGGAGAACTGGGATGTG 445
QY 421 TACAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTACTGATGAGAACCAAC 480
DB 446 TACAGGTGATCTATTATTAAGATGGTGAAGTCTTCAAGTACTGATGAGAACCAAC 505
QY 481 ATCTCCATTACAAATGCCACAGTGTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 540
DB 506 ATCTCCATTACAAATGCCACAGTGTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTG 565
QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591
DB 566 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 616

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RESULT 5

```

US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match      100.0%; Score 591; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 5.7e-183;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 60
DB 107 ATGGCTCTCGCATGGAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 166
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTTGAACCCCTCCATGGAATAGA 120
DB 167 GATGGCGTGTAGCAGTCCCTCAGAAACCTTAGGTCCTTGAACCCCTCCATGGAATAGA 226
QY 121 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 180
DB 227 ATATTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGT 286
QY 181 TCACCAAAATGTTCCAAATGCGAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 240
DB 287 TCACCAAAATGTTCCAAATGCGAGCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATATT 346
QY 241 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACGACCAACCAAGTTTAATGAG 300
DB 347 GTGAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTGACGACCAACCAAGTTTAATGAG 406

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QY 301 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTTCAGGCTCTGCTGAG 360  
DB 407 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTTCAGGCTCTGCTGAG 466  
QY 361 GTGGTGTAGAGGGCCAGCCCTCTTCCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 420  
DB 467 GTGGTGTAGAGGGCCAGCCCTCTTCCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTG 526  
QY 421 TACAAGGTGTATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480  
DB 527 TACAAGGTGTATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 586  
QY 481 ATCTCCATTACAATGCCACAGTGAAGAGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 540  
DB 587 ATCTCCATTACAATGCCACAGTGAAGAGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 646  
QY 541 TGGCAGCTGACATGATGCTGTAGCCCTCAACATTAATATAAAGCT 591  
DB 647 TGGCAGCTGACATGATGCTGTAGCCCTCAACATTAATATAAAGCT 697

RESULT 6

US-09-944-277A-3/C  
; Sequence 3, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-3505  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1198 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-944-277A-3

Query Match 100.0%; Score 591; DB 9; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 5.7e-183;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 60  
DB 1092 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 1033  
QY 61 GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 120  
DB 1032 GATGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGA 973  
QY 121 ATATTTAAAGAGAGAGATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGT 180  
DB 972 ATATTTAAAGAGAGAGATGTGACTCTTACATGTAAATGGGAAACAATTTCTTTGAAGTCAGT 913  
QY 181 TCCACCAATGGTTCCACAATGGCAGCCCTTTTCAGAAAGAGACAAATTCAGTTTCAATATT 240  
DB 912 TCCACCAATGGTTCCACAATGGCAGCCCTTTTCAGAAAGAGACAAATTCAGTTTCAATATT 853  
QY 241 GTGAATGCCAAATTTTGAAGAGACAGTGGAGAAATACAAATGTCAACCAACCAAGTTAATGAG 300  
DB 852 GTGAATGCCAAATTTTGAAGAGACAGTGGAGAAATACAAATGTCAACCAACCAAGTTAATGAG 793  
QY 301 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTTCAGGCTCTTTCGCTGAG 360  
DB 792 AGTGAACCTGTGTACTGGAAGTCTTCACTGACTGGCTGCTCTTTCAGGCTCTTTCGCTGAG 733  
QY 361 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 420  
DB 732 GTGGTGTATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTG 673  
QY 421 TACAAGGTGTATCTATTATTAAGGATGGTGAAGCTCTTCACTGACTGGCTGCTCTTTCAGGCTCTTTCGCTGAG 480  
DB 672 TACAAGGTGTATCTATTATTAAGGATGGTGAAGCTCTTCACTGACTGGCTGCTCTTTCAGGCTCTTTCGCTGAG 613  
QY 481 ATCTCCATTACAATGCCACAGTTCGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 540  
DB 612 ATCTCCATTACAATGCCACAGTTCGAAGACAGTGGAACTACTACTGTACGGGCAAGTG 553  
QY 541 TGGCAGCTGGAATGATGACTCTGAGCCCTCAACATTAATATAAAGCT 591  
DB 552 TGGCAGCTGGAATGATGACTCTGAGCCCTCAACATTAATATAAAGCT 502

RESULT 7

US-09-962-832-244  
; Sequence 244, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal  
; FILE REFERENCE: 689290-74  
; CURRENT APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,077  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,280  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 244  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-962-832-244

Query Match 100.0%; Score 591; DB 9; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 5.7e-183;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 60  
DB 107 ATGGCTCTGCGCATGGAAATCCCTACTACTGTGTGTAGCTTACTGTCTTTCGCTCCA 166

QY 61 GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCCCTCCATGGAATAGA 120  
 DB 167 GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCCCTCCATGGAATAGA 226  
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGT 180  
 DB 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGT 286  
 QY 181 TCACCAATGTTCCACAAATGCGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATT 240  
 DB 287 TCACCAATGTTCCACAAATGCGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATT 346  
 QY 241 GTCAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAAGCAACCAAGTTAATGAG 300  
 DB 347 GTCAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAAGCAACCAAGTTAATGAG 406  
 QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 360  
 DB 407 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 466  
 QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420  
 DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526  
 QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGGAACCAAC 480  
 DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGGAACCAAC 586  
 QY 481 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTCTGTAACGGCAAGTG 540  
 DB 587 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTCTGTAACGGCAAGTG 646  
 QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591  
 DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 697

RESULT 8  
 US-10-775-169-141  
 ; Sequence 141, Application US/10775169  
 ; Publication No. US2004017543A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Burczynski, Michael  
 ; APPLICANT: Twine, Natalie  
 ; APPLICANT: Dornier, Andrew  
 ; APPLICANT: Trepicchio, William  
 ; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
 ; FILE REFERENCE: AM101080 (031896-013000)  
 ; CURRENT APPLICATION NUMBER: US/10/775,169  
 ; CURRENT FILING DATE: 2004-02-11  
 ; NUMBER OF SEQ ID NOS: 5278  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 141  
 ; LENGTH: 1198  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-775-169-141

Query Match 100.0%; Score 591; DB 17; Length 1198;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-183;  
 Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 60  
 DB 107 ATGGCTCTGCCATGGAATCCCTACTCTACTGTGTAGCTTACTGTCTTCTGCTCCA 166  
 QY 61 GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCCCTCCATGGAATAGA 120  
 DB 167 GATGGCGGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAAACCCCTCCATGGAATAGA 226  
 QY 121 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGT 180

DB 227 ATATTTAAAGGAGAGAAATGTGACTCTTACATGTAATGGAACAATTTCTTTGAAGTCAGT 286  
 QY 181 TCACCAATGTTCCACAAATGCGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATT 240  
 DB 287 TCACCAATGTTCCACAAATGCGAGCCTTTCAGAAAGAGACAAATTCAGTTTGAATATT 346  
 QY 241 GTCAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAAGCAACCAAGTTAATGAG 300  
 DB 347 GTCAATGCCAAATTTGAAGACAGTGGAGAAATACAAATGTCAAGCAACCAAGTTAATGAG 406  
 QY 301 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 360  
 DB 407 AGTGAACCTGTGTACCTGGAAGTCTTTCAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAG 466  
 QY 361 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420  
 DB 467 GTGGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526  
 QY 421 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGGAACCAAC 480  
 DB 527 TACAAGGTGATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGGTATGGAACCAAC 586  
 QY 481 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTCTGTAACGGCAAGTG 540  
 DB 587 ATCTCCATTACAAATGCCACAGTTGAGACAGTGGAACTTACTCTGTAACGGCAAGTG 646  
 QY 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591  
 DB 647 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 697

RESULT 9  
 US-09-944-277A-12  
 ; Sequence 12, Application US/09944277A  
 ; Patent No. US20020034771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank, Glenn R.  
 ; APPLICANT: Porter, James P.  
 ; APPLICANT: Rushlow, Keith E.  
 ; APPLICANT: Wassom, Donald L.  
 ; TITLE OF INVENTION: Method to Detect Ige  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ; STREET: 1825 Sharp Point Drive  
 ; CITY: Fort Collins  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80525  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: WordPerfect for Windows, Version 7.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/944,277A  
 ; FILING DATE: 30-Aug-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/285,873  
 ; FILING DATE: 1999-03-31  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Verser, Carol Talkington  
 ; REGISTRATION NUMBER: 37,459  
 ; REFERENCE/DOCKET NUMBER: DI-1  
 ; TELEPHONE: 970/493-7272  
 ; TELEFAX: 970/484-9505  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 516 nucleotides  
 ; TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..516  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-944-277A-12

Query Match 87.3%; Score 516; DB 9; Length 516;  
Best Local Similarity 100.0%; Pred. No. 1.5e-158;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 135  
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 60  
QY 136 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195  
Db 61 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGTAATGCAATTTT 255  
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGTAATGCAATTTT 180  
QY 256 GAAGCAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 315  
Db 181 GAAGCAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 316 CTGGAAGTCTTCAAGTACTGGTCTCCTTCAAGCCCTCTGCTGAGGTGGTGGAGGGC 375  
Db 241 CTGGAAGTCTTCAAGTACTGGTCTCCTTCAAGCCCTCTGCTGAGGTGGTGGAGGGC 300  
QY 376 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGCACTGGGATGTGTACAAAGGTGATCTAT 435  
Db 301 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGCACTGGGATGTGTACAAAGGTGATCTAT 360  
QY 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495  
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
QY 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555  
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591  
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 11  
US-09-809-715-1  
Sequence 1, Application US/0909715  
Publication No. US20030003502a1  
GENERAL INFORMATION:  
APPLICANT: Jardetzky, Theodore S.  
APPLICANT: Garman, Scott Clayton  
APPLICANT: Wurzburg, Beth A.  
APPLICANT: Kinet, Jean-Pierre  
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC  
TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A PC REGION OF AN IGE  
FILE REFERENCE: AL-8  
CURRENT APPLICATION NUMBER: US/09/809,715  
CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/189,853  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 1  
LENGTH: 528  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(528)

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..516  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-944-277A-12

Query Match 87.3%; Score 516; DB 9; Length 516;  
Best Local Similarity 100.0%; Pred. No. 1.5e-158;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 135  
Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCCCTCATGGAATAGATATTTAAAGGAGAG 60  
QY 136 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195  
Db 61 AATGTGACTCTTACATGTAAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGTAATGCAATTTT 255  
Db 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATTTGTAATGCAATTTT 180  
QY 256 GAAGCAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 315  
Db 181 GAAGCAGTGGAGATACAAATGTGAGCAGCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 316 CTGGAAGTCTTCAAGTACTGGTCTCCTTCAAGCCCTCTGCTGAGGTGGTGGAGGGC 375  
Db 241 CTGGAAGTCTTCAAGTACTGGTCTCCTTCAAGCCCTCTGCTGAGGTGGTGGAGGGC 300  
QY 376 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGCACTGGGATGTGTACAAAGGTGATCTAT 435  
Db 301 CAGCCCTCTTCTCAGTGGCCTGCTGAGGAGCACTGGGATGTGTACAAAGGTGATCTAT 360  
QY 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495  
Db 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
QY 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555  
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
QY 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591  
Db 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 10  
US-10-293-992-3  
Sequence 3, Application US/10293992  
Publication No. US20040033527a1  
GENERAL INFORMATION:  
APPLICANT: Jardetzky, Theodore S.  
APPLICANT: Garman, Scott Clayton  
APPLICANT: Kinet, Jean-Pierre  
TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A PC EPSILON RECEPTOR  
TITLE OF INVENTION: CHAIN  
FILE REFERENCE: AL-3-C1-1  
CURRENT APPLICATION NUMBER: US/10/293,992  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: 09/434,193  
PRIOR FILING DATE: 1999-11-04  
PRIOR APPLICATION NUMBER: 60/107,219  
PRIOR FILING DATE: 1998-11-05  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 3  
LENGTH: 516  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-809-715-1

Query Match 87.3%; Score 516; DB 10; Length 528;

Best Local Similarity 100.0%; Pred. No. 1.5e-158;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 135  
 DB 1 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 60  
 QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 195  
 DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120  
 QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 255  
 DB 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180  
 QY 256 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315  
 DB 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
 QY 316 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGC 375  
 DB 241 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGC 300  
 QY 376 CAGCCCTCTTCTCAGTGGCCATGGTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 435  
 DB 301 CAGCCCTCTTCTCAGTGGCCATGGTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360  
 QY 436 TATAGGATGGTGAAGCTCTCAAGTACTGGTGTGAGACCAACCAATCTCCATTACAAAT 495  
 DB 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTGTGAGACCAACCAATCTCCATTACAAAT 420  
 QY 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGGTGTCGAGCTGGACTAT 555  
 DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGGTGTCGAGCTGGACTAT 480  
 QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
 DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

RESULT 12

US-10-293-992-1

; Sequence 1, Application US/10293992

; Publication No. US20040033527A1

; GENERAL INFORMATION:

; APPLICANT: Jaretsky, Theodore S.

; APPLICANT: Garman, Scott Clayton

; APPLICANT: Kinet, Jean-Pierre

; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR

; TITLE OF INVENTION: CHAIN

; FILE REFERENCE: AL-3-C1-1

; CURRENT APPLICATION NUMBER: US/10/293.992

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/434,193

; PRIOR FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: 60/107,219

; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 1

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(528)

; OTHER INFORMATION:

US-10-293-992-1

Query Match

87.3%; Score 516; DB 13; Length 528;

Best Local Similarity 100.0%; Pred. No. 1.5e-158;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 135  
 DB 1 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGATAATTTAAAGGAG 60  
 QY 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 195  
 DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTCCACCAATGGTTC 120  
 QY 196 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 255  
 DB 121 CACAATGGCAGCCTTTTCAAGAGAGACAATTTCAAGTTTGAATATTTGTAATGCCAAATTT 180  
 QY 256 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315  
 DB 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
 QY 316 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGC 375  
 DB 241 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAAGGCTCTGCTGAGGTGGTGTGAGGGC 300  
 QY 376 CAGCCCTCTTCTCAGTGGCCATGGTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 435  
 DB 301 CAGCCCTCTTCTCAGTGGCCATGGTGGAGGAACCTGGATGTGTACAAGTGTATCTAT 360  
 QY 436 TATAGGATGGTGAAGCTCTCAAGTACTGGTGTGAGACCAACCAATCTCCATTACAAAT 495  
 DB 361 TATAGGATGGTGAAGCTCTCAAGTACTGGTGTGAGACCAACCAATCTCCATTACAAAT 420  
 QY 496 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGGTGTCGAGCTGGACTAT 555  
 DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGGTGTCGAGCTGGACTAT 480  
 QY 556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
 DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516

RESULT 13

US-09-944-277A-7

; Sequence 7, Application US/09944277A

; Patent No. US20020034771A1

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Porter, James P.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect IGE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..699  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-944-277A-7

Query Match 87.3%; Score 516; DB 9; Length 699;  
Best Local Similarity 100.0%; Pred. No. 1.8e-158;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 76 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 135  
Db 1 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60  
QY 136 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 195  
Db 61 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120  
QY 196 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 255  
Db 121 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180  
QY 256 GAAGACAGTGGGAATACAAATGTCAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 315  
Db 181 GAAGACAGTGGGAATACAAATGTCAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 316 CTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGAGAGGC 375  
Db 241 CTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGAGAGGC 300  
QY 376 CAGCCCTCTTCTCAGTGGCTGCTGCTGAGGAACTGGGATGTGACAGGTGATCTAT 435  
Db 301 CAGCCCTCTTCTCAGTGGCTGCTGCTGAGGAACTGGGATGTGACAGGTGATCTAT 360  
QY 436 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 495  
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420  
QY 496 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 555  
Db 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480  
QY 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591  
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516

RESULT 14  
US-09-909-715-3  
Sequence 3, Application US/09809715  
Publication No. US2003003502A1  
GENERAL INFORMATION:  
APPLICANT: Jaretzky, Theodore S.  
APPLICANT: Garman, Scott Clayton  
APPLICANT: Wurzburg, Beth A.  
APPLICANT: Kinet, Jean-Pierre  
TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A PC  
TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN IGE  
TITLE OF INVENTION: ANTIBODY AND USES THEREOF  
FILE REFERENCE: AL-8  
CURRENT APPLICATION NUMBER: US/09/809,715

CURRENT FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/189,853  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 528  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(528)  
US-09-809-715-3  
Query Match 85.1%; Score 503.2; DB 10; Length 528;  
Best Local Similarity 98.4%; Pred. No. 2.5e-154;  
Matches 508; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 76 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 135  
Db 1 GTCCTCAGAAACCTAAGTCTCCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAG 60  
QY 136 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 195  
Db 61 AATGTGACTCTTACATGTAATGGCAACAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120  
QY 196 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 255  
Db 121 CACAATGGCAGCCTTTTCAGAAAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180  
QY 256 GAAGACAGTGGGAATACAAATGTCAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 315  
Db 181 GAAGACAGTGGGAATACAAATGTCAGCAACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 316 CTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGAGAGGC 375  
Db 241 CTGGAAGTCTTTCAGTGAAGTGGCTGCTCTTTCAGGCTCTGCTGAGTGGTGTGAGAGGC 300  
QY 376 CAGCCCTCTTCTCAGTGGCTGCTGCTGAGGAACTGGGATGTGACAGGTGATCTAT 435  
Db 301 CAGCCCTCTTCTCAGTGGCTGCTGCTGAGGAACTGGGATGTGACAGGTGATCTAT 360  
QY 436 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 495  
Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420  
QY 496 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 555  
Db 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480  
QY 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591  
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516

RESULT 15  
US-10-236-392-29  
Sequence 29, Application US/10236392  
Publication No. US20040067490A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Burgess, Catherine, E  
APPLICANT: Casman, Stacie J  
APPLICANT: Catterton, Elina  
APPLICANT: Chapoval, Andrei  
APPLICANT: Crabtree, Julie  
APPLICANT: Edinger, Shlomit, R  
APPLICANT: Ellerman, Karen  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Grosche, William M  
APPLICANT: Gusev, Vladimir

APPLICANT: Kekuda, Ramesh  
APPLICANT: LaRoche, William J  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Miller, Charles E  
APPLICANT: Millett, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol A  
APPLICANT: Peyman, John A  
APPLICANT: Rastelli, Luca  
APPLICANT: Reiger, Daniel K  
APPLICANT: Rothenberg, Mark E  
APPLICANT: Shenoy, Suresh  
APPLICANT: Shinkets, Richard A  
APPLICANT: Smithson, Glenn  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-442A  
CURRENT APPLICATION NUMBER: US/10/236,392  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US09/540,763  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: US60/390,155  
PRIOR FILING DATE: 2002-06-19  
PRIOR APPLICATION NUMBER: US09/635,949  
PRIOR FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: US60/318,765  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US60/357,303  
PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: US60/367,753  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: US60/369,479  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US09/559,634  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: US60/318,120  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: US60/318,130  
PRIOR FILING DATE: 2001-09-07  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 794  
SOFTWARE: Custom  
SEQ ID NO 29  
LENGTH: 757  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (26)..(680)  
US-10-236-392-29

Query Match  
Best Local Similarity 58.7%; Score 347; DB 13; Length 757;  
Matches 474; Conservative 0; Mismatches 0; Indels 117; Gaps 1;  
Pred. No. 7e-103;

Qy 1 ATGGCTCTGGCAGTAAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 60  
Db 26 ATGGCTCTGGCAGTAAATCCCTACTCTACTGTGTGTAGCCTTACTGTCTTCGCTCCA 85  
Qy 61 GATGGCTGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 120  
Db 86 GATGGCTGTGTAGCAGTCCCTCAGAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGA 145  
Qy 121 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180  
Db 146 ATATTAAAGAGAGAAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 205  
Qy 181 TCCACCAAAATGGTTCCCAATGGCGCTTTTCAGAGAGACAAATTCAGTTTGATATT 240  
Db 206 TCCACCAAAATGGTTCCCAATGGCGCTTTTCAGAGAGACAAATTCAGTTTGATATT 265

Qy 241 GTGAATGCCAAATTTGAAGACAGAGTGGAGAAATACAAATGTACACACCAACAAAGTTAATGAG 300  
Db 266 GTGAATGCCAAATTTGAAGACAGAGTGGAGAAATACAAA----- 301  
Qy 301 AGTGAACCTGTGTACCTGGAAAGTCTTTCAGTGACTGGCTCTCTTCAGGCCCTCTCTGTGAG 360  
Db 302 ----- 301  
Qy 361 GTGGTATGAGGGGCCAGCCCTCTTCTCTCAGTGCCATGGTTGAGGAACCTGGGAATGTG 420  
Db 302 -----TGGCATGGTTGGAGGAACCTGGGAATGTG 328  
Qy 421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGGTATGAGAACCAAC 480  
Db 329 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGGTATGAGAACCAAC 388  
Qy 481 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG 540  
Db 389 ATCTCCATTACAAATGCCACAGTTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTG 448  
Qy 541 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591  
Db 449 TGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 499

Search completed: October 11, 2004, 01:41:41  
Job time : 344.307 secs

OM nucleic - nucleic search, using sw model

Run on:	October 10, 2004, 11:14:29	; Search time 1994.19 Seconds (without alignments)
		8949.962 Million cell updates/sec

Run on: October 10, 2004, 11:14:29 ; Search time 1994.19 Seconds  
(without alignments)

**Title:** US-10-763-400-10  
**Perfect score:** 591  
**Sequence:** 1 atgqctctgccatgaatc.....acattactgtataaaagct 591

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

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Minimum DB seg length: 0
Maximum DB seg length: 200000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : EST:*
          1: em estba:*
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3: em_estn: *
4: em_estmu: *
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em_estpl:*
6:
em_estro:*
7:

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9:  gb_est1: *
10: gb_est2: *

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12: gb_esc3: *
13: gb_esc4: *

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15: em_estfun: *
16: em_estrom: *

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18: em_gss_inv:*
19: em_gss_pln:*
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21: em_gss_fun: *
22: em_gss_mam: *
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24: em_gss_pro: *
25: em_gss_rtd: *
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27: em_gss_vr1:*
28: gb_gss1:*
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Pred. No. is the number of results predicted by chance to have a

and is derived by analysis of the total score distribution.

Result	Query
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[illegible]

## ALIGNMENTS

RESULT 1	ACCESSION	REFERENCE
LOCUS	VERSION	AUTHORS
DEFINITION	KEYWORDS	TITLE
	SOURCE	JOURNAL
	ORGANISM	COMMENT

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 60257205F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4696381 5',  
 mRNA sequence.  
 BG542554  
 BG542554.1 GI:13534787  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Primates; Catarrhini; Homnidae; Homo.  
 Mammalia; Eutheria;

1 (bases 1 to 810)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [rcapbs@mail.nih.gov](mailto:rcapbs@mail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI523 row: h column: 14  
 High quality sequence stop: 667







Db 151 ATATTTAAAGGAGAGATGACTCTTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 210  
 Qy 181 TCACCAAAATGGTTCCACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 240  
 Db 211 TCACCAAAATGGTTCCACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATT 270  
 Qy 241 GTGAATCCAAATTTGAAGACAGTGGAGATACAAATGTTCAGCACCACCAAGTAAATGAG 300  
 Db 271 GTGAATCCAAATTTGAAGACAGTGGAGATACAAATGTTCAGCACCACCAAGTAAATGAG 330  
 Qy 301 AGTCAACCTGTGTACCTGGAAAGTCTTCAGTACATGGCTGTCTCTCAGGCTCTGTCTGAG 360  
 Db 331 AGTCAACCTGTGTACCTGGAAAGTCTTCAGTACATGGCTGTCTCTCAGGCTCTGTCTGAG 390  
 Qy 361 GTGTGTATGAGAGCCAGCCCTCTCTCCTCAGTGCATCGTTGGAGGAATCGGATGTG 420  
 Db 391 GTGTGTATGAGAGCCAGCCCTCTCTCCTCAGTGCATCGTTGGAGGAATCGGATGTG 450  
 Qy 421 TACAAGCTGTCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 480  
 Db 451 TACAAGCTGTCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAAC 510  
 Qy 481 ATCTCCATTACAAAT--GCCACAGTTGAAGACAGTGGAACTAC-TACTGTACGGGCAAA 537  
 Db 511 ATCTCCATTACAAATGGCCACAGTTTGAAGACAGTGGAACTACTTACTGTACGGGCAAA 570  
 Qy 538 GTGTGGCAGCTGGAC 552  
 Db 571 GTGTGGCAGCTGGAC 585

BF678252 846 bp mRNA linear EST 21-DEC-2000  
 602086161F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4250222 5',  
 mRNA sequence.  
 BF678252  
 BF678252.1 GI:11952147  
 EST.  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

RESULT 4  
 BF678252  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 846)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1071 row: j column: 15  
 High quality sequence stop: 609.  
 Location/Qualifiers  
 1..846  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4250222"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 83"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgctcgcc); Site 2: SfiI  
 (ggcgctcgcc); 5' and 3' adaptors were used in cloning  
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'  
 and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGCGCCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.4

FEATURES  
 Source

Db 451 TACAAGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAA- 509  
 Qy 481 ATCTCCATTACAAATGGCAGTGGAGACAGTGGAACTACTACTGTACGGGCAAGTG 540  
 Db 510 ATCTCCATTACAAATGGCAGTGGAGACAGTGGAACTACTACTGTACGGGCAAGTG 569  
 Qy 541 TGGCAGCTGGATGATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591  
 Db 570 TGGCAGCTGGATGATGAGTCTGAG-CCCTCAACATTACTGTAAATAAAGCT 619

BG548515 840 bp mRNA linear EST 04-APR-2001  
 602576508F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4704624 5',  
 mRNA sequence.  
 BG548515  
 BG548515.1 GI:13547180  
 EST.  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 840)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM1544 row: p column: 01  
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 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:  
 SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctcgcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGCGCCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 86.3%; Score 509.8; DB 12; Length 840;  
 Best Local Similarity 97.3%; Pred. No. 3.3e-140;  
 Matches 540; Conservative 12; Indels 3; Gaps 2;

Qy 1 ATGGCTCTCCGATGGATCCCTACTCTACTGTGTAGCTTCTTCTTCTGCTCCA 60  
 Db 31 ATGGCTCTCCGATGGATCCCTACTCTACTGTGTAGCTTCTTCTTCTGCTCCA 90  
 Qy 61 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGTGAACCTCCATGGAATAGA 120  
 Db 91 GATGGCTGTGTAGCAGTCCCTCAGAAACCTTAAGTCTCTTGTGAACCTCCATGGAATAGA 150  
 Qy 121 ATATTTAAAGGAGAGATGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGTCAGT 180



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 818)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLC1074 row: n column: 14  
High quality sequence stop: 616.  
Location/Qualifiers

FEATURES  
source

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/db\_xref="taxon:9606"  
/clone="IMAGE:4251469"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_83"  
/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfII (ggccctggcc); Site 2: SfII  
(ggccattggcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'  
and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGGCGGCATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.4  
Kb (range 0.5-4.0 Kb). 14/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA)."

ORIGIN

Query Match 65.9%; Score 389.4; DB 10; Length 818;  
Best Local Similarity 88.9%; Pred. No. 2.3e-104;  
Matches 536; Conservative 0; Mismatches 51; Indels 16; Gaps 10;

QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTAGCCCTACTGTCTTTCGCTCCA 60  
DB 35 ATGGCTCTGCGAAGGAATCCCTACTCTACTGTGTAGCCCTACTGTCTTTCGCTCCA 94  
QY 61 GATGGCGTTAGCAGTCCTCTGAAACCTTAAGTCTCTTGAACCCCTCATGGAATAGA 120  
DB 95 GATGGCGTTAGCAGTCCTCTGAAACCTTAAGTCTCTTGAACCCCTCATGGAATAGA 154  
QY 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTT-TGAAGTCAG 179  
DB 155 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTT-TGAAGTCAG 214  
QY 180 TTCCACCAATGGTTCCCAATGGCAGCCCTTTCAGAAAGAGACAATTCAGTTTGAATA- 238  
DB 215 TTCCACCAATGGTTCCCAATGGCAGCCCTTTCAGAAAGAGACAATTCAGTTTGAATA 274  
QY 239 ---TTGTGAATGCCAAAT--TTGAAGACAGTGGAGAT-ACAATGTGCGACCAACAAG 292  
DB 275 TACTGGTGAATGCCAAATTTGGAAGACAGTGGCGGAATAACAATGTGCGACCAACAAG 334  
QY 293 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCGCT 352  
DB 335 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAAGTGGCTCTCTTCAGGCGCT 394  
QY 353 CTGCTGAGGTGGTGAAGGGCCAGCCCTCTTCCTCAGGTGGCAGTGGTGGAGAACT 412  
DB 395 CTGCTGAGGTGGTGAAGGGCCAGCCCTCTTCCTCAGGTGGCAGTGGTGGAGAAC 454  
QY 413 GGGATGCTAC-AAGGTGATCTATTATAAGATGGTGAAGCTCTCAAGTACTGTATGAG 471  
DB 455 TGGATGTGTACAAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACT-GTATGAG 513

QY 472 AACCAACATCTCCATTACAATGCGACAGTGTGAACAGAGTGAACCC---TACTACTGT 528  
DB 514 AACCA-AAAATTTCCATTACAATGCGACAGTGTGAACAGAGTGAACCCAACTAATCTGT 572  
QY 529 ACGGGCAAA-GTGTGGCAGCTGGACTA-TGAGTCTGAGCCCTCAACATTAATTAATAA 586  
DB 573 ACGGGCAAAAGTGTGGCAAGTGGACTATTGAGTCTTGAGCCCTCAACATTAATTA 632  
QY 587 AAG 589  
DB 633 AAG 635

RESULT 7  
CF362072 829457 MARC 3PIG Sus scrofa cDNA 5', mRNA linear EST 25-AUG-2003  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Sus scrofa (pig)  
Sus scrofa  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 660)  
Smith,T.P.L., Freking,B.A., Ford,J.J., Valliet,J.L., Fox,J.,  
Wise,T.A., Nonnenman,D.J., Wray,J.E. and Keele,J.W.  
A second set of porcine ESTs from a pooled-tissue normalized  
library

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.950329.  
Plate: SRG8018 row: L column: 4  
Seq primer: GTAATACGACTCCTATAGG.

FEATURES  
source

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Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3PIG"  
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including brain, liver, muscle, placenta/endometrium,  
ovary, testes, and bone marrow."

ORIGIN

Query Match 56.7%; Score 335; DB 14; Length 660;  
Best Local Similarity 72.9%; Pred. No. 3.1e-88;  
Matches 431; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 1 ATGGCTCTGCGATGGAAATCCCTACTCTACTGTGTAGCCCTACTGTCTTTCGCTCCA 60  
DB 16 ATGTCTACTCCCATAGGAGTCCCTGCTGTATGATAGTCTGCTGCTCTCTCTCCA 75  
QY 61 GATGGCGTGTAGCAGTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCAATGAATAGA 120  
DB 76 GATGGCATGGCAGCAGTCAATCCAGGAATCTCAGGTGCTCTTGAATCCCATGAATAGA 135  
QY 121 ATATTTAAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGT 180  
DB 136 ATATTTAGAGGAGAGATGTGACTCTTACATGTAATGGGAACAATTTGAATATAC 195  
QY 181 TCACCAAAATGGTTCCCAATGGCAGCCCTTTCAGAAAGAGACAATTCAGTTTGAATAT 240

Db 196 CCCACCAATTGGACACACACCAAACTTTTGGAGTGAATACTTCGAGTTGGGACCTT 255  
 QY 241 GTGAATGCCAAATTTTGAAGACAGTGGAGATACAAATGTGACGCCAACCAAGTTAATGAG 300  
 Db 256 AAGAATGCAAAACCTGGGACAGCGGCAATACAGATGCCAAGCAAGACTTTTACATG 315  
 QY 301 AGTGAACCTGTGTACTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 360  
 Db 316 AGTGAACCTGTGTACTGGAAGTCTTCAGTGAAGTGGCTGCTCTTCAGGCTCTGCTGAG 375  
 QY 361 GTGGTGTGAGGAGGCGGAGCCCTCTTCCTCAGGTGCCATGTTGGAGAACTGGGATGTG 420  
 Db 376 GTGGTGTGAGGAGGCGGAGCTCTCTCTCTCATGTGTGACGCTGGAAGATCTGAATGTC 435  
 QY 421 TACAAGGTGATCTTATTAAGATGGTGAAGCTCTCAAGTACTGATGAGAACCAAC 480  
 Db 436 TATAAGGTGATCTTACTAAGGATGGCAAGCCCTCAAGTACTGATGAGAACCAAC 495  
 QY 481 ATCTCCATTACAAATGCCACAGTTCGAAGACAGTGGAACTACTACTGTGACGGCAAGTG 540  
 Db 496 CTCTCCATTACCAATGCCAAGAGAGACAGTGGCTCTTATTTGTCACCGGCTAATT 555  
 QY 541 TGGCAGCTGGATGATGATGCTGAGCCCTCAACATTAATGTAATAAAGCT 591  
 Db 556 CAAAAAATACCAAAAACTCTACTACTCTCACCATTACATACAAACAGAT 606

## RESULT 8

BQ573778/c  
 LOCUS BQ573778 768 bp mRNA linear EST 19-JUN-2002  
 DEFINITION UI-H-E20-bav-1-04-0-UI-s1 NCI CGAP Chl Homo sapiens cDNA clone  
 UI-H-E20-bav-1-04-0-UI 3', mRNA sequence.  
 ACCESSION BQ573778  
 VERSION BQ573778.1 GI:21477095  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 768)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. Steven Gitelis/ Rush Prebiterian, Dept. of  
 Orthopedics  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, [bento-soares@iowa.edu](mailto:bento-soares@iowa.edu)  
 The following repetitive elements were found in this cDNA  
 sequence: 1-41, >AT-rich#low complexity (matched complement)  
 93-129, >LINE2 (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

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 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone="UI-H-E20-bav-1-04-0-UI"  
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 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP Chl"  
 /note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)  
 with a modified polylinker; Site: 1: Ecor I; Site: 2: Not I;  
 NCI CGAP Chl is a cDNA library containing the following  
 tissue(s): Chondrosarcoma Grade II. The library was  
 constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an Ecor I  
 adapter, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 TGATCAGCT.  
 TAG\_ISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=UI-H-E20  
 TAG\_SEQ=ATCTAATATG

## ORIGIN

Query Match 49.7%; Score 294; DB 13; Length 768;  
 Best Local Similarity 99.7%; Pred. No. 5.6e-76;  
 Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 297 TGAGAGTGAACCTGTGTACTTGAAGTCTTCAAGTGAAGTGGCTCTTCAGGCTCTGCG 356  
 Db 768 TGAGAGTGAACCTGTGTACTTGAAGTCTTCAAGTGAAGTGGCTCTTCAGGCTCTGCG 709  
 QY 357 TGAGTGTGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGA 416  
 Db 708 TGAGTGTGTGATGGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGGA 649  
 QY 417 TGTGTACAGGTGATCTATTATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCA 476  
 Db 648 TGTGTACAGGTGATCTATTATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCA 589  
 QY 477 CAACATCTCCATTACAAATGCCACAGTTCGAACAGTGGAACTACTACTGTACGGGCAA 536  
 Db 588 CAACATCTCCATTACAAATGCCACAGTTCGAACAGTGGAACTACTACTGTACGGGCAA 529  
 QY 537 AGTGTGGCAGCTGGAGTATGATGCTGAGCCCTCAACATTAATGTAATAAAGCT 591  
 Db 528 AGTGTGGCAGCTGGAGTATGATGCTGAGCCCTCAACATTAATGTAATAAAGCT 474

## RESULT 9

BY752906 652 bp mRNA linear EST 17-DEC-2002  
 BY752906 RIKEN full-length enriched, adult inner ear Mus musculus  
 cDNA clone F930034C11 5', mRNA sequence.  
 BY752906  
 EST. GI:27184082  
 Mus musculus (house mouse)

## LOCUS

DEFINITION BY752906  
 ACCESSION BY752906  
 VERSION BY752906.1  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 652)

## AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaide, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schenbach, C., Gojibori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,  
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Mikhi, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Sempie, C.A., Secou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, W.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Yoshihide Hayashizaki  
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Tel: 81-45-503-9222

Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Konno, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

source

Location/Qualifiers

1. .652  
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/mol\_type="mRNA"  
/strain="C57BL/6J"  
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/clone="F930034C11"  
/tissue\_type="inner ear"  
/dev\_stage="adult"  
/clone\_lib="RIKEN full-length enriched, adult inner ear"

## ORIGIN

Query Match Similarity 46.1%; Score 272.6; DB 13; Length 652;  
Best Local Similarity 68.6%; Pred. No. 1.2e-69;  
Matches 406; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

QY 3 GGCTCTCCATGGAATCCCTACTCTGTGTGAGCCCTTACTGTCTTCGCTCCAGA 62  
DB |||||  
29 GCGATGTCTACTGGAAGTCTGCCAGCTGTGCTAGCACTGTCTCTCTCTGTA 88  
DB |||||  
63 TGGCGTGTAGAGTCCCTCAGAACCTTAAGGTCTCTTGACCTCCATCGATAGAT 122  
DB |||||  
89 TGTCACTTGACGCACTGAGAAATCTGTACTGACCTTGGACCCACCATGATTAAT 148  
DB |||||

QY 123 ATTTAAAGGAGAGATGTGACTCTTACATGTAATGGGAAACAATTTCTTTGAAGT---CAG 179  
DB 149 ATTTACAGGAGAGAAAGTGACCCCTTTCTCTGTATGGGAAACAATCCCTTCAATGAATC 208  
QY 180 TTCCACCAATATGTTTCCAAATGCGACCCCTTTAGAGAGACAAATTCAGATTTGAATAT 239  
DB 209 TACTACTAAATGGATCCAAATGTTACCGTCTCTGAGGTGAACCTCTTCAACATTTGGTCAT 268  
QY 240 TGTGAATGCCAAATTTGAAGACAGTGGAGAAATCAAAATGTGAGCAACCAACGAATTAATGA 299  
DB 269 TGTGATGCCACCGTTCAAGACAGTGGAAATACATATGTCAGAAAGCAAGATTGTTAA 328  
QY 300 GAGTGAACCTGTGTACCTGGAAGTCTTCAGTGAATGCTCTCTCAGGCTCTGCTGA 359  
DB 329 GAGTAAACCTGTGTACTTGAATGTAACCAAGATTGGTCTCTCTCAGACATCTGCTGA 388  
QY 360 GGTGTGATGAGGCGCCAGCCCTCTCTCCTCAGTGGCCATGCTTGGAGGAACCTGGATGT 419  
DB 389 CATGATCTTAGTCCATGATCTCTTGACATCAGATGCCATGGCTGGAGAACTGGAATGT 448  
QY 420 GTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAACCAAA 479  
DB 449 CGCAAGGTGATCTACTACAGGAATGACCATGCTTTCAACTACAGTTATGAGAGCC---C 505  
QY 480 CATCTCCATTACAATGCCACAGTGGAGACAGTGGACCTTACTCTACCGGCAAAAGT 539  
DB 506 COTCTCCATTAGAGAGGCCACACTGAATGACAGTGGACCTTACCCTGNCAGGGCTATCT 565  
QY 540 GTGGCAGCTGGACATGATGCTGAGCCCTCAACATTTACTCTTAATAAAGCT 591  
DB 566 TAGGAGGTGGAATGATCTGACAAATTCAGAAATGCTGTAGTAAAGCT 617

CA448745 707 bp mRNA linear EST 08-NOV-2002  
UI-H-E10-ayo-p-24-0-UI.s1 NCI CGAP E10 Homo sapiens cDNA clone  
UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.  
CA448745  
VERSION 1  
GI:24813165  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 707)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jose Mercuende  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
The following repetitive elements were found in this cDNA  
sequence: 93-129, >LINE2 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1. .707  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-E10-ayo-p-24-0-UI"  
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/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP E10"  
/note="Organ: Left Pelvis, Vector: pT7T3-Pac (Pharmacia)"

with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP E10 is a cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag located between the Not I site and the (GT)18 tail. The sequence tag for this library is ACACCTGGCAC.

TAG\_TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-E10  
TAG\_SEQ=ACACCTGGCAC

## ORIGIN

Query Match 39.6%; Score 234; DB 14; Length 707;  
Best Local Similarity 100.0%; Pred. No. 3.9e-58;  
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 GAGGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTGGAT 417  
|||||  
Db 707 GAGGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTGGAT 648  
|||||  
QY 418 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATGAGAACAC 477  
|||||  
Db 647 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTCTGATGAGAACAC 588  
|||||  
QY 478 AACATCTCCATTAACAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGGCAAA 537  
|||||  
Db 587 AACATCTCCATTAACAATGCCACAGTTGAACACAGTGGAACTACTACTGTACGGGCAAA 528  
|||||  
QY 538 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591  
|||||  
Db 527 GTGTGGCAGCTGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 474  
|||||

## RESULT 11

CA419024/c  
LOCUS 712 bp mRNA linear EST 07-NOV-2002  
DEFINITION UI-H-E21-bbj-e-19-0-UI s1 NCI CGAP\_Ch2 Homo sapiens cDNA clone  
UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.

ACCESSION CA419024  
VERSION CA419024.1 GI:24781675  
KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapb-remail.nih.gov](mailto:cgapb-remail.nih.gov)

Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of Orthopedics

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)

The following repetitive elements were found in this cDNA

sequence: 1-42, >(TAAAA)n#Simple repeat (matched complement)

94-130, >LINE2 (matched complement)

Seq primer: M13 FORWARD

POLYA=Yes

## FEATURES

source

1..712

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-H-E21-bbj-e-19-0-UI"

/tissue\_type="Chondrosarcoma Grade II"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI CGAP\_Ch2"

/notes="Organ: Left Pelvis; Vector: pTV73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP\_Ch2 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTV73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is ACACCTGGCACCT.

TAG\_TISSUE=grade-2-chondrosarcoma

TAG\_LIB=UI-H-E21

TAG\_SEQ=ATCTAATATG

## ORIGIN

Query Match 38.7%; Score 228.6; DB 14; Length 712;  
Best Local Similarity 97.1%; Pred. No. 1.6e-56;  
Matches 231; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 354 TGCTGAGGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTG 413  
|||||  
Db 712 TGCTGAGGTGGTGTGAGGGCCAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACCTG 653  
|||||  
QY 414 GGATGTGTACAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAA 473  
|||||  
Db 652 GGATGTGTACAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTATGAGAA 593  
|||||  
QY 474 CCACAACATCTCCATTACAATGCCACAGTGGAACTACTACTGTACCGG 533  
|||||  
Db 592 CCACAACATCTCCATTACAATGCCACAGTGGAACTACTACTGTACCGG 533  
|||||  
QY 534 CAAAGTGGCGAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 591  
|||||  
Db 532 CAAAGTGGCGAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 475  
|||||

## RESULT 12

AW357271 394 bp mRNA linear EST 25-APR-2001  
LOCUS 40240 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION AW357271

VERSION AW357271.1 GI:6861277

KEYWORDS EST.

SOURCE Bos taurus (cow)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.

1 (bases 1 to 394)

Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Caas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,

Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,

Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F.,

Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282378

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366





ALPHA-SUBUNIT (HUMAN);, mRNA sequence.  
 AW612525  
 VERSION  
 AW612525.1 GI:7317711  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 669)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 438.  
 Location/Qualifiers  
 1..669  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2954053"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid11"  
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Plasmid DNA from the normalized library NCI-CGAP Kid3 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library.  
 (clone)Ds 1322376-1323911, 1456007-1456775, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldi."
 

Query Match 33.6%; Score 198.8; DB 10; Length 669;  
 Best Local Similarity 96.2%; Pred. No. 1.1e-47;  
 Matches 203; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 391 CCTCTTCTCCAGTGGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTATTATAA 440  
 Db 669 CCTCTTCTCCAGTGGCCATGTTGGAGAACTGGATGTGTACAGGTGATCTATTATAA 610  
 QY 441 GGATGGTGAAGCTCTCAAGTACTGATGACCAACCAACATCTCCATTACAAATGCCAC 500  
 Db 609 GGATGGTGAAGCTCTCAAGTACTGATGACCAACCAACATCTCCATTACAAATGCCAC 550  
 QY 501 AGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGGCAGCTGGACTATGAGTC 560  
 Db 549 AGTTGAAGACAGTGGAACTACTACTGTACGGGCAAGTGGCAGCTGGACTATGAGTC 560  
 QY 561 TGAGCCCTCAACATTACTGTATATAAAGCT 591  
 Db 489 TGAGCCCTCAACATTACTGTATATAAAGCT 459

RESULT 15  
 CB768694  
 LOCUS  
 DEFINITION  
 AB000001:SRP2-00228-E10-A srpb2 (10220) Rattus norvegicus cDNA  
 clone srpb2-00228-e10 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 CB768694.1 GI:29857085

EST.  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 403)  
 Angen EST Program.  
 Angen Rat EST Program  
 Unpublished (2003)  
 Contact: Dan Fitzpatrick  
 Angen, Inc  
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00228 row: e column: 10.  
 Location/Qualifiers  
 1..403  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="srpb2-00228-e10"  
 /tissue\_type="prostate tissue"  
 /clone\_lib="srpb2 (10220)"  
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; rat  
 prostate normalized double selected poly(A+) mRNA size  
 fraction > 1 kb"
 

Query Match 29.7%; Score 175.6; DB 14; Length 403;  
 Best Local Similarity 69.9%; Pred. No. 6.6e-41;  
 Matches 235; Conservative 0; Mismatches 101; Indels 0; Gaps 0;  
 QY 256 GAAGACAGTGGAGATACAAATGTCAGCACCACCAAGTTATGAGTGAACCTGTGTAC 315  
 Db 11 GAAGACAGTGGAGATACAAATGTCAGCACCACCAAGTTATGAGTGAACCTGTGTAC 70  
 QY 316 CTGGAAGTCTTCAGTCACTGGCTGCTCCTTCAGGCTCTGCTGAGGTGGTGTGAGGGC 375  
 Db 71 TTGAACNTGATCGANGAGTGGCTGCTGCTCCTCAATCTTCTGCTGAGGTGGTGTGAG 130  
 QY 376 CAGCCCTCTTCTCAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435  
 Db 131 GGATCCTTTGACATCAGATCGGCTAGCTGGAAGAAATGGAAGTCCCAAGGTGATCTAC 190  
 QY 436 TATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAACATCTCCATTACAAAT 495  
 Db 191 TACAGGACGACATGCTTTCAAGTACTCTTATGACAGCAACACATCTCCATTAGAAAG 250  
 QY 496 GCCACAGTTGAAGACAGTGGAACTTACTTACTGTCAGGGCAAGTGTGGCAGCTGACTAT 555  
 Db 251 GCCACATTTAATGACAGTGGCAGCTTCCACTGTCAGGCTATTTTGAACAGAGTTGAATGT 310  
 QY 556 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 591  
 Db 311 AAATCTGATAATTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346

Search completed: October 10, 2004, 19:44:39  
 Job time : 1995.19 secs



GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 44.5431 Seconds  
(without alignments)  
1249.617 Million cell updates/sec

Title: US-10-763-400-11  
Perfect score: 1073  
Sequence: 1 MAPAMSPPTLLCVALLFFAP.....GKVMQDYSEPLNITVIKA 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	2 AAR45778	Human dih
2	1073	100.0	197	4 AAB31586	A Fc epsi
3	1073	100.0	235	2 AAR26064	Human FcE
4	1073	100.0	257	1 AAP90385	Alpha sub
5	1073	100.0	257	2 AAR05025	Alpha sub
6	1073	100.0	257	2 AAR14772	Human Fc(
7	1073	100.0	257	2 AAR42336	Human Fce
8	1073	100.0	257	2 AAR24066	Alpha sub
9	1073	100.0	257	2 AAW61190	The alpha
10	1073	100.0	257	2 AAW48094	Human Ige
11	1073	100.0	257	4 AAB74667	Human imm
12	1073	100.0	257	4 AAB31584	Amino aci
13	1073	100.0	257	5 AAB32801	Human Ige
14	1073	100.0	257	6 ABO01301	Human pro
15	1073	100.0	257	7 ADB85536	Human imm
16	1073	100.0	257	7 ADD48674	Human pro
17	1073	100.0	260	3 AAY96230	Human Fc
18	1073	100.0	660	4 AAB31593	Fc epsilo
19	1073	100.0	756	4 AAB31590	Amino aci
20	1073	100.0	978	2 AAW48096	Human ser
21	1073	100.0	978	5 AAG32803	Human Ige
22	1032	96.2	193	2 AAR89281	Ige high
23	962.5	99.7	247	2 AAR30483	Human hig
24	953	88.8	183	3 AAY96232	Recombina
25	951	88.6	182	3 AAY96234	Recombina

26	947	88.3	172	2 AAY33185	Aay33185 Human sFc
27	947	88.3	172	3 AAY94211	Aay94211 Human PhF
28	947	88.3	172	4 AAB31587	Aab31587 A Fc epsi
29	947	88.3	176	3 AAY94210	Aay94210 Human PhF
30	947	88.3	176	4 AAG65597	Ag65597 Amino aci
31	947	88.3	232	4 AAB31585	Aab31585 Amino aci
32	947	88.3	635	4 AAB31594	Aab31594 Fc epsilo
33	947	88.3	731	4 AAB31591	Aab31591 Amino aci
34	922	85.9	176	4 AAG65598	Ag65598 Amino aci
35	840.5	78.3	218	6 ABO01302	Ab001302 Human pro
36	775	72.2	281	2 AAR13867	Aar13867 Hybrid Fc
37	679	63.3	281	2 AAR13870	Aar13870 Hybrid Fc
38	639	59.6	281	2 AAR13872	Aar13872 Fc(gamma)
39	617	57.5	201	2 AAY27061	Aay27061 Recombina
40	617	57.5	255	2 AAY27058	Aay27058 Equine Fc
41	606	56.5	281	2 AAR13869	Aar13869 Hybrid Fc
42	595	55.5	190	5 AAE18631	Aae18631 Equine hi
43	584	54.4	236	2 AAY27060	Aay27060 Equine Fc
44	554	51.6	199	2 AAW81111	Aaw81111 Canine Fc
45	545	50.8	197	2 AAW81115	Aaw81115 Canine Fc

## ALIGNMENTS

RESULT 1  
AAR45778  
ID AAR45778 standard; protein; 197 AA.  
XX  
AC AAR45778;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-SEP-1994 (first entry)  
XX  
DE Human dihydrofolate reductase (DHFR).  
XX  
KW Dihydrofolate reductase; DHFR; marker; transformation.  
XX  
OS Homo sapiens.  
XX  
PN WO9403598-Al.  
XX  
PD 17-FEB-1994.  
XX  
PF 03-AUG-1993; 93WO-JP001085.  
XX  
PR 04-AUG-1992; 92JP-0029227.  
PR 10-AUG-1992; 92JP-00213002.  
PR 08-OCT-1992; 92JP-00270513.  
PR 08-OCT-1992; 92JP-00270514.  
PR 08-OCT-1992; 92JP-00270515.  
XX  
(GREC ) GREEN CROSS CORP.  
PI Ra C, Naito K, Hirama M, Okumura K;  
DR WPI; 1994-065687/08.  
DR N-PSDB; AAQ55369.  
XX  
PT Antiallergic peptide derived from high-affinity immunoglobulin E receptor  
FT - binds to human immunoglobulin E to block allergic reactions at source.  
PS Disclosure; Page 24-25; 37pp; Japanese.  
XX  
CC The dihydrofolate reductase (DHFR) gene was used in the construction of a  
CC vector as a selectable marker. The resulting vector was used to transform  
CC DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 2; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.3e-77;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFEVS 60  
 |||||  
 Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFEVS 60  
 |||||  
 QY 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVPSDWLLQLQASAE 120  
 |||||  
 Db 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVPSDWLLQLQASAE 120  
 |||||  
 QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
 |||||  
 Db 121 VMWEGQPLFLRCHGWRNWDVYKVIYYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
 |||||  
 QY 181 WOLDYESEPLNITVIKA 197  
 |||||  
 Db 181 WOLDYESEPLNITVIKA 197  
 |||||  
 RESULT 2  
 AAB31586  
 ID AAB31586 standard; protein; 197 AA.  
 XX  
 AC AAB31586;  
 DT 30-APR-2001 (first entry)  
 XX  
 DE A Fc epsilon receptor alpha-chain extracellular domain.  
 XX  
 KW Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IGE; atopic disease;  
 KW luminescence inducing protein; allergy; hyper IGE syndrome;  
 KW internal parasite infection; B cell neoplasia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200104310-A1.  
 XX  
 PD 19-JAN-2001.  
 XX  
 PF 13-JUL-2000; 2000WO-US019070.  
 XX  
 PR 13-JUL-1999; 99US-0143612P.  
 PR 02-MAR-2000; 2000US-0186412P.  
 XX  
 PA (HESKA-) HESKA CORP.  
 PA (PROM-) PROMEGA CORP.  
 XX  
 PI Weber ER, Wood KV, Hall MP;  
 XX  
 XX WPI; 2001-103082/11.  
 DR N-PSDB; AAF24915.  
 XX  
 PT A fusion protein, comprising an Fc epsilon receptor domain and a  
 PT luminescence inducing protein domain that induces a LP substrate to emit  
 PT light when contacted with the LP domain, useful for detecting  
 PT immunoglobulin (Ig) E.  
 XX  
 PS Claim 16; Page 65; 105pp; English.  
 XX  
 CC The present sequence represents the extracellular domain of a human Fc  
 CC epsilon receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds  
 CC to immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a  
 CC fusion protein, which also comprises a luminescence inducing protein  
 CC domain that induces a substrate to emit light when contacted with the  
 CC luminescence inducing protein domain. The fusion protein may be used to  
 CC detect IgE. It may also be used to identify a compound capable of  
 CC inhibiting Fc epsilonR protein activity. IGE antibody production is  
 CC indicative of diseases such as allergies, atopic disease, hyper IGE  
 CC syndrome, internal parasite infections and B cell neoplasia. Detection of  
 CC IGE production in an animal following therapy is indicative of the  
 CC efficacy of the treatment, for example when using treatments intended to  
 CC disrupt IGE production  
 XX  
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 4; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFEVS 60  
 |||||  
 Db 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPNRRIFKGENVTLCNGNFFEVS 60  
 |||||  
 QY 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVPSDWLLQLQASAE 120  
 |||||  
 Db 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVPSDWLLQLQASAE 120  
 |||||  
 QY 121 VMWEGQPLFLRCHGWRNWDVYKVIYYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
 |||||  
 Db 121 VMWEGQPLFLRCHGWRNWDVYKVIYYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
 |||||  
 QY 181 WOLDYESEPLNITVIKA 197  
 |||||  
 Db 181 WOLDYESEPLNITVIKA 197  
 |||||  
 RESULT 3  
 AAR26064  
 ID AAR26064 standard; protein; 235 AA.  
 XX  
 AC AAR26064;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 DE Human Fc epsilon alpha-subunit and IL-2 hybrid protein.  
 XX  
 KW High affinity Fc immunoglobulin E receptor; IGE; antibody; interleukin-2;  
 KW histamine release; allergy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 26..201  
 FT /label= human\_FcERI\_alpha-subunit  
 FT /note= "epitope recognised by new Mab"  
 XX  
 XX BP499112-A1.  
 XX  
 PD 19-AUG-1992.  
 XX  
 PF 03-FEB-1992; 92EP-00101732.  
 XX  
 PR 11-FEB-1991; 91US-00653936.  
 XX  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA  
 XX Chizsonite RA, Hakimi J, Kochan JP;  
 PI  
 XX WPI; 1992-277871/34.  
 DR  
 XX  
 PT Monoclonal antibodies bind to alpha sub-unit of Fc IGE receptor - for  
 PT treatment and prevention of IGE induced allergic diseases, also for  
 PT measuring alpha sub-unit and IGE levels in biological fluids.  
 XX  
 PS Disclosure; Page 8; 30pp; English.  
 XX  
 CC This is a preferred protein for use in generating the monoclonal  
 CC antibodies of the invention. The protein comprises an epitope of the  
 CC human Fc epsilon alpha-subunit to which the cytoplasmic and transmembrane  
 CC regions of the IL-2 receptor have been fused. (Cytoplasmic and  
 CC transmembrane regions from receptors other IL-2 receptor can be also  
 CC used). The specification includes a nucleotide coding sequence which is a  
 CC preferred fusion gene (see AAQ27267); the polypeptide which is decoded  
 CC from that fusion gene differs from the amino acid sequence AAR26064 as  
 CC follows: amino acids 5-7 are Arg-Ile-Leu (not Met-Glu-Ser), amino acid  
 CC 209 is Cys (not Lys), amino acid 229 is Ser (not Arg), Arg233 is absent

CC and an additional C-terminal amino acid (Phe) is present. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 235 AA;

Query Match 100.0%; Score 1073; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5.2e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120  
 DB 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120

QY 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180  
 DB 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

QY 181 WLDYSEPLNITVIKA 197  
 DB 181 WLDYSEPLNITVIKA 197

RESULT 4

AAP90385

ID AAP90385 standard; protein; 257 AA.

XX

AC AAP90385;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 01-NOV-1989 (first entry)

XX

XX Alpha subunit of human mast cell IgE surface receptor.

XX

XX Immunoglobulin E receptor alpha subunit; allergies;

XX non-peptide drug design; human.

XX

XX Homo sapiens; (Human); mast cell line.

OS KU812.

XX

XX WO8905352-A.

XX

PD 15-JUN-1989.

XX

XX 29-NOV-1988; 88WO-US004255.

XX

XX 01-DEC-1987; 87US-00127214.

XX

XX (HARD ) HARVARD COLLEGE.

PA (USSH ) NAT INST OF HEALTH.

XX

XX Leder P, Benfey P;

PI

XX

XX WPI; 1989-192698/26.

DR N-PSDB; AAP90126.

XX

XX CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.

FT

XX

XX Disclosure; Fig 4; 17pp; English.

PS

XX

XX Immunoglobulin E receptor alpha subunit of human mast cell IgE surface receptor (see corresp. AAP90126). Used to produce antibodies which can diagnose IGE receptor levels measure and treat allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

XX

XX Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 5.8e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120  
 DB 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDDLLOASAE 120

QY 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180  
 DB 121 VMEGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYICTGKV 180

QY 181 WLDYSEPLNITVIKA 197  
 DB 181 WLDYSEPLNITVIKA 197

RESULT 5

AAR05025

ID AAR05025 standard; protein; 257 AA.

XX

AC AAR05025;

XX

XX 02-OCT-1990 (first entry)

XX

DE Alpha subunit of human high affinity IgE receptor.

XX

XX high affinity IgE receptor; alpha subunit of IgE receptor; human;

KW allergic response; ss.

XX

XX Synthetic.

XX

XX WO9004640-A.

XX

XX 03-MAY-1990.

XX

XX 18-OCT-1988; 88US-00259065.

XX

XX 18-OCT-1988; 88US-00259065.

XX

XX (USDC ) US SEC OF COMMERCE.

XX

XX Kinest JP, Metzger H;

PI

XX

XX WPI; 1990-164023/21.

DR N-PSDB; AAQ04644.

XX

XX DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and derived polypeptides, for therapy and diagnosis of allergies, and studies of IgE receptor interaction.

PT

XX

XX Disclosure; Page ?; -pp; English.

PS

XX

XX The high affinity receptor is a tetrameric complex consisting of 2 gamma subunits and one each of subunits alpha and beta. It is expressed on mast cells and is involved in the allergic response. COS-7 cells cotransfected with cDNA for all 3 intact subunit types (derived from rat basophilic leukaemia cells) express receptor on their surfaces. Detailed study of the receptors is now possible. See also AAQ04643 and AAQ04645-6

XX

XX Sequence 257 AA;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFFAPDGLVAVPQPKVSLNPPNRIKGENVTITCNGNNFFEVS 60

Query Match 100.0%; Score 1073; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 5.8e-77;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 STKWFHNGSLSEETNSLNINAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLQLQASAE 120  
 DB 61 STKWFHNGSLSEETNSLNINAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLQLQASAE 120  
 QY 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180  
 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180  
 QY 181 WOLDYSEPLNITVIKA 197  
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 6  
 AAR14772  
 ID AAR14772 standard; protein; 257 AA.  
 XX AAR14772;  
 XX 25-MAR-2003 (revised)  
 DT 17-DEC-2001 (revised)  
 DT 03-FEB-1992 (first entry)  
 XX Human Fc(epsilon)RI alpha subunit.  
 DE Immunoglobulin; receptor; high affinity receptor.  
 XX Homo sapiens.  
 XX Location/Qualifiers  
 FH Key 1..25  
 FT Peptide /label= signal  
 FT Protein 26..257  
 FT /label= alpha\_subunit  
 FT Domain 80..104  
 FT /label= homologous domain  
 FT /note= "homologous to residues 163-190"  
 FT Domain 163..190  
 FT /label= homologous domain  
 FT /note= "homologous to residues 80-104"  
 FT Region 205..224  
 FT /label= transmembrane  
 FT Region 225..257  
 FT /label= cytoplasmic  
 XX USN7626704-N.  
 XX 15-OCT-1991.  
 XX 14-DEC-1990; 90US-00626704.  
 XX 14-DEC-1990; 90US-00626704.  
 XX (USSH ) NAT INST OF HEALTH.  
 XX Kinet JP, Metzger H;  
 XX WPI; 1991-346755/47.  
 XX N-PSDB; AAQ14736.  
 XX DNA coding alpha, beta and gamma-units of ige high affinity receptor -  
 PT are used to prepare recombinant polypeptide(s) for treating allergy, drug  
 PT screening or monitoring IGE level.  
 XX Disclosure; Fig 1; 58pp; English.  
 XX A lambda gt11 library was prepared from poly-A RNA isolated from KUB12  
 CC cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha  
 CC cDNA corresponding to nucleotides 119-781. Positive clones were subcloned  
 CC and sequenced. This amino acid sequence was deduced from the cDNA clone.  
 CC (Note: Revised entry submitted to correct the patent number format of US  
 CC Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent

CC web site at www.derwent.com/dwpi/updates/ntis\_us.html.) (Updated on 25-  
 CC MAR-2003 to correct PF field.)  
 XX Sequence 257 AA;  
 SQ

Query Match 100.0%; Score 1073; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGLAVPOKPKVSLNPPNRRIFKGENVTLTCGNNGFFVS 60  
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPOKPKVSLNPPNRRIFKGENVTLTCGNNGFFVS 60  
 QY 61 STKWFHNGSLSEETNSLNINAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLQLQASAE 120  
 DB 61 STKWFHNGSLSEETNSLNINAKPEDSGEYKCOHQVNESEPPVYLEVFSWLLQLQASAE 120  
 QY 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180  
 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKV 180  
 QY 181 WOLDYSEPLNITVIKA 197  
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 7  
 AAR42336  
 ID AAR42336 standard; protein; 257 AA.  
 XX AAR42336;  
 XX 25-MAR-2003 (revised)  
 DT 21-JUN-1994 (first entry)  
 XX Human FcεRI alpha.  
 DE IgE; immunoglobulin E receptor; beta subunit; basophils; allergy;  
 KW aggregation; signal transduction; diagnosis; antagonist.  
 XX Homo sapiens.  
 XX WO9321317-A1.  
 XX 28-OCT-1993.  
 XX 16-APR-1993; 93WO-US003419.  
 XX 16-APR-1992; 92US-00869933.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX Kinet JP;  
 XX WPI; 1993-351727/44.  
 XX N-PSDB; AAQ51020.  
 XX Immunoglobulin E receptor human beta sub-unit isolation - using 1st  
 PT strand reverse transcripts from human basophils as templates for a  
 PT polymerase chain reaction, used to treat and diagnose allergic diseases.  
 XX Claim 5; Fig 1; 154pp; English.  
 XX The sequence is that of the human FcεRI alpha subunit, isolated by using  
 CC first strand reverse transcriptase from human basophils by PCR. The gene  
 CC and its prod. can be used to identify human beta subunit FcεRI inhibitors  
 CC (immunoglobulin E receptor) which inhibit the binding of IgE to its  
 CC receptor and inhibit the aggregation function of the receptor or the  
 CC signal transducing function related to allergic response. Such inhibitors  
 CC can be used for the treatment or prevention of allergic disease. See also  
 CC AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 257 AA;  
 SQ

Query Match 100.0%; Score 1073; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIFKGENVTILTCGNNFFEVS 60  
DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIFKGENVTILTCGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120  
DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120

QY 121 VMMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
DB 121 VMMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180

QY 181 WQDYSESEPLNITVIKA 197  
DB 181 WQDYSESEPLNITVIKA 197

RESULT 8  
AAW24066  
ID AAW24066 standard; protein; 257 AA.

XX AC AAW24066;  
XX DT 04-FEB-1998 (first entry)

XX DE Alpha subunit of human high affinity receptor for IgE (human FcERI).  
XX KW alpha subunit; human high affinity receptor; IgE; FcERI; antigen;  
XX KW performed mediator; histamine; serotonin; leukotriene; IgE level;  
XX KW allergic condition; therapy; allergic response; drug screening;  
XX KW DNA probe; diagnostic assay.  
XX OS Homo sapiens.

XX PH Key Location/Qualifiers  
FT Peptide 1..225 /label= signal\_peptide  
FT Protein 26..257 /label= mature\_peptide  
FT Region 26..204 /label= extracellular\_portion\_of\_protein  
FT Domain 80..104 /label= homologous\_domain\_1  
FT /note= "this region is homologous with amino acids 163-190"  
FT Domain 163..190 /label= homologous\_domain\_2  
FT /note= "this region is homologous with amino acids 80-104"  
FT Region 205..224 /label= transmembrane\_segment  
FT Region 225..257 /label= cytoplasmic\_domain

XX US5639660-A.  
XX 17-JUN-1997.  
XX 24-FEB-1988; 88US-00160457.  
XX 24-FEB-1988; 88US-00160457.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX (HOFF ) HOFFMANN LA ROCHE INC.  
XX Kochan JP, Kinet JP;  
XX WPI; 1997-332052/30.

DR N-PSDB; AAT85615.  
XX DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin  
XX E - used for producing polypeptide(s) which can be used for therapy or to  
XX prevent allergic responses or in diagnostic and screening assays.  
XX Claim 7; Fig 1A-B; 15pp; English.  
XX This sequence represents the alpha subunit of the human high affinity  
XX receptor for IgE (FcERI). FcERI is found exclusively on mast cells,  
XX basophils and related cells. Aggregation of IgE occupied FcERI by antigen  
XX triggers both the release of of preformed mediators such as histamine and  
XX serotonin, as well as stimulating the synthesis of leukotrienes. It is  
XX the release of these mediators that results in an allergic condition. The  
XX DNA can be used to produce the human FcERI alpha polypeptides which can  
XX be used for therapy or to prevent allergic responses. In drug screening  
XX assays or for monitoring IgE levels in patients. The DNA encoding this  
XX protein can also be used to produce DNA probes useful in diagnostic  
XX assays  
XX Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIFKGENVTILTCGNNFFEVS 60  
DB 1 MAPAMESPTLLCVALLFFAPDGLVAPQPKVSLNPPNRIFKGENVTILTCGNNFFEVS 60

QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120  
DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEFPVYLEVFSWMLLQASAE 120

QY 121 VMMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180  
DB 121 VMMEGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180

QY 181 WQDYSESEPLNITVIKA 197  
DB 181 WQDYSESEPLNITVIKA 197

RESULT 9  
AAW61190  
ID AAW61190 standard; protein; 257 AA.

XX AC AAW61190;  
XX DT 07-OCT-1998 (first entry)

XX DE The alpha chain of a Fc epsilon receptor.  
XX KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;  
XX KW immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;  
XX KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;  
XX KW flea allergy; heartworm infection.  
XX OS Homo sapiens.  
XX PN WO9823964-A1.  
XX PD 04-JUN-1998.  
XX PF 24-NOV-1997; 97WO-US021651.  
XX PR 26-NOV-1996; 96US-00756387.  
XX PA (HESK-) HESKA CORP.  
XX PI Frank RG, Porter JP, Rushlow KE, Wassom DL;  
XX WPI; 1998-322873/28.

DR N-PSDB; AAV36343.  
 XX  
 XX Detection of non-human immunoglobulin E - by complex formation with human  
 PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic  
 PT disease.  
 XX  
 XX  
 PS Disclosure; Page 37-38; 70pp; English.  
 XX  
 XX The present sequence represents the alpha chain of the human Fc epsilon  
 CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)  
 CC comprises reacting isolated human Fc epsilon receptor with the test  
 CC sample and detecting formation of a IgE-receptor complex. Detection of  
 CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,  
 CC internal parasitic infections or B cell neoplasia, and for measuring  
 CC effect of treatments. Most particularly flea allergy in dogs and cats is  
 CC detected, and also heartworm infection  
 XX  
 SQ Sequence 257 AA;  
 Query Match 100.0%; Score 1073; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQKPKVSLNPPNRIKGENVTLTCNGNPFVS 60  
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQKPKVSLNPPNRIKGENVTLTCNGNPFVS 60  
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDDLQASAE 120  
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDDLQASAE 120  
 QY 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
 DB 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
 QY 181 WOLDYESEPLNITVIKA 197  
 DB 181 WOLDYESEPLNITVIKA 197  
 RESULT 10  
 ID AAW48094 standard; protein; 257 AA.  
 XX  
 AC AAW48094;  
 XX  
 DT 20-JUL-1998 (first entry)  
 XX  
 DE Human IgE receptor Fc-epsilon-RI alpha chain.  
 XX  
 KW Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;  
 KW fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;  
 KW eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= Sig\_peptide  
 FT /label= Mat\_protein  
 FT Domain 26..204  
 FT /note= "extracellular domain"  
 XX  
 PN WO9804718-A1.  
 XX  
 PD 05-FEB-1998.  
 XX  
 XX 25-JUL-1997; 97WO-EP004066.  
 XX  
 PR 26-JUL-1996; 96US-00690216.  
 XX  
 FA (NOVS ) NOVARTIS AG.

XX  
 PI Digan ME, Lake P, -Gram H;  
 XX  
 DR WPI; 1998-130705/12.  
 DR N-PSDB; AAV20402.  
 XX  
 PT New fusion polypeptide for, e.g. diagnosing allergies - comprises  
 PT immunoglobulin E-binding domain fused to human serum albumin.  
 XX  
 PS Claim 2; Page 44; 77pp; English.  
 XX  
 CC This is the amino acid sequence of the dominant form of full-length  
 CC native human IgE receptor Fc-epsilon RI alpha chain. A claimed fusion  
 CC protein (FP) comprises an IgE binding domain fused to at least one human  
 CC serum albumin (HSA) component (see AAW38095), optionally via a peptide  
 CC linker, and is especially a dimeric FP (see AAW48096) comprising HSA  
 CC fused, at each of its N- and C-termini, to the extracellular domain of Fc  
 CC -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP  
 CC (see AAV20404); a vector; a process for preparing the FP; a method of  
 CC performing gene therapy in humans that comprises removing somatic cells  
 CC from a patient, genetically modifying them in culture by insertion of a  
 CC polynucleotide that encodes the FP, and reintroducing the modified cells  
 CC into the patient so that the FP is expressed by the cells of the patient;  
 CC and use of the FP in an in vitro diagnostic assay to determine the level  
 CC of IgE or auto-antibodies to Fc epsilon RI in a sample. The products can  
 CC be used in the prevention and/or treatment of IgE-mediated allergic  
 CC diseases and related disorders such as atopic dermatitis, atopic asthma,  
 CC chronic urticaria, hayfever and eczema. Compared with using IgE binding  
 CC domain alone, the FP has a longer serum life, and thus greater activity,  
 CC without a loss of ability to bind serum IgE or circulating auto-  
 CC antibodies  
 XX  
 SQ Sequence 257 AA;  
 Query Match 100.0%; Score 1073; DB 2; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQKPKVSLNPPNRIKGENVTLTCNGNPFVS 60  
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQKPKVSLNPPNRIKGENVTLTCNGNPFVS 60  
 QY 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDDLQASAE 120  
 DB 61 STKWFHNGSLSEETNSSLNIVNAKFDGSEYKCOHQVNESEPVYLEVFSDDLQASAE 120  
 QY 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
 DB 121 VMGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
 QY 181 WOLDYESEPLNITVIKA 197  
 DB 181 WOLDYESEPLNITVIKA 197  
 RESULT 11  
 AAB74667  
 ID AAB74667 standard; protein; 257 AA.  
 XX  
 AC AAB74667;  
 XX  
 DT 19-JUN-2001 (first entry)  
 XX  
 DE Human immunoglobulin E receptor I alpha subunit protein.  
 XX  
 KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;  
 KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;  
 KW immunoassay; detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200111010-A2.  
 XX

PD 15-FEB-2001.  
 XX  
 XX 02-AUG-2000; 2000WO-US021097.  
 XX  
 XX 09-AUG-1999; 99US-0147860P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 XX  
 XX Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;  
 PI Stephens JC;  
 XX  
 XX WPI; 2001-202766/20.  
 DR N-PSDB; AAF97964.  
 XX  
 XX New polynucleotide for gene therapy, comprises nucleotide polymorphisms  
 PT in the immunoglobulin E receptor I alpha subunit gene.  
 PT  
 XX  
 XX Claim 10; Fig 3; 99pp; English.  
 XX  
 XX The present invention describes an isolated polynucleotide (I) comprising  
 CC a nucleotide sequence (S) which is a polymorphic variant of a reference  
 CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)  
 CC gene or its fragment. The polymorphic variant comprises at least one  
 CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,  
 CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine  
 CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at  
 CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide  
 CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at  
 CC a position corresponding to nucleotide 530. (I) can be used in gene  
 CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)  
 CC encoded by (I) is useful in drug screening assays and in assays to  
 CC measure the binding affinity of one or more candidate drugs targeting  
 CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from  
 CC solution and also reacts with (II) on Western or immunoblots of  
 CC polyacrylamide gels on membrane supports or substrates. (III) is also  
 CC useful in immunoassays to detect (II) in biological samples. AAF97965 to  
 CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097  
 CC to AAF98140 represent IGERA gene polymorphism detection primers; and  
 CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in  
 CC the exemplification of the present invention. The present sequence  
 CC represents the human IGERA protein used in the present invention  
 XX  
 XX Sequence 257 AA;  
 SQ  
 Query Match 100.0%; Score 1073; DB 4; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60  
 QY 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEBPVYLEVFSDWLLQASAE 120  
 DB 61 STKWFHNGSLSEETNSLNINAKFEDSGEYKCOHQVNESEBPVYLEVFSDWLLQASAE 120  
 QY 121 VVMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180  
 DB 121 VVMEGQPLFLRCHGWRNDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180  
 QY 181 WQDYSEPLNITVIKA 197  
 DB 181 WQDYSEPLNITVIKA 197  
 RESULT 12  
 AAB31584  
 ID AAB31584 standard; protein; 257 AA.  
 XX  
 XX AAB31584;  
 XX  
 XX 30-APR-2001 (first entry)  
 DT  
 XX

DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.  
 XX  
 XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;  
 KW luminescence inducing protein; allergy; hyper IgE syndrome;  
 KW internal parasite infection; B cell neoplasia.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200104310-A1.  
 PN  
 XX 18-JAN-2001.  
 PD  
 XX 13-JUL-2000; 2000WO-US019070.  
 PF  
 XX 13-JUL-1999; 99US-0143612P.  
 PR 02-MAR-2000; 2000US-0186412P.  
 XX  
 XX (HESK-) HESKA CORP.  
 PA (PROM-) PROMEGA CORP.  
 XX  
 XX Weber ER, Wood KV, Hall MP;  
 PI  
 XX WPI; 2001-103082/11.  
 DR N-PSDB; AAF24911.  
 XX  
 XX A fusion protein, comprising an Fc epsilon receptor domain and a  
 PT luminescence inducing protein domain that induces a LP substrate to emit  
 PT light when contacted with the LP domain, useful for detecting  
 PT immunoglobulin (Ig) E.  
 XX  
 XX Claim 16; Page 60; 105pp; English.  
 PS  
 XX The present sequence represents a human Fc epsilon receptor (Fc epsilonR)  
 CC alpha-chain protein, that binds to immunoglobulin (Ig) E. The Fc epsilonR  
 CC domain is used to produce a fusion protein, which also comprises a  
 CC luminescence inducing protein domain that induces a substrate to emit  
 CC light when contacted with the luminescence inducing protein domain. The  
 CC fusion protein may be used to detect IgE. It may also be used to identify  
 CC a compound capable of inhibiting Fc epsilonR protein activity. IgE  
 CC antibody production is indicative of diseases such as allergies, atopic  
 CC disease, hyper IgE syndrome, internal parasite infections and B cell  
 CC neoplasia. Detection of IgE production in an animal following therapy is  
 CC indicative of the efficacy of the treatment, for example when using  
 CC treatments intended to disrupt IgE production  
 XX  
 XX Sequence 257 AA;  
 SQ  
 Query Match 100.0%; Score 1073; DB 4; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIKGENVTLCNGNFFEVS 60  
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 DB 181 WQDYSEPLNITVIKA 197  
 RESULT 13  
 ABG32801  
 ID ABG32801 standard; protein; 257 AA.  
 XX  
 XX ABG32801;  
 AC

XX 29-NOV-2002 (first entry)

DE Human IgE receptor FcpepsilonRIalpha.

XX Human; IgE; receptor; FcpepsilonRIalpha; HSA; human serum albumin;  
 KW anti-allergic; dermatological; anti-inflammatory; antiasthmatic;  
 KW IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;  
 KW atopic dermatitis; atopic asthma; chronic urticaria.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal\_peptide

FT Region /label= Mature\_FcpepsilonRIalpha

FT /label= IgE\_binding\_domain

FT /note= "This region is specifically claimed in claim 5"

XX US6423512-B1.

XX 23-JUL-2002.

XX 21-JUL-1997; 97US-00897956.

XX 26-JUL-1996; 96US-0022689P.

XX (NOVS ) NOVARTIS AG.

XX Digan ME, Lake P, Gram H;  
 WPI; 2002-672940/72.  
 DR N-PSDB; ABS2959.

XX New fusion IgE-binding polypeptide, useful for the prevention and  
 PT treatment of systemic allergy and/or other IgE-receptor-mediated  
 PT disorders such as atopic dermatitis, atopic asthma and chronic urticaria.

XX Claim 5; Fig 13; 49pp; English.

XX The invention relates to a new fusion polypeptide or its pharmaceutically  
 CC acceptable salt comprises at least one IgE-binding domain fused to at  
 CC least one human serum albumin (HSA) component, where the IgE-binding  
 CC domain is the sequence (a) defined residues Val26-Leu204 of the protein  
 CC sequence appearing as ABG32801, or a truncation at the carboxy terminus  
 CC by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined  
 CC by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a  
 CC polynucleotide sequence encoding the fusion protein; (3) a host cell  
 CC transformed with the polynucleotide; (4) a method of preparing the fusion  
 CC protein comprising transforming a host cell with a vector comprising a  
 CC polynucleotide encoding the fusion polypeptide, expressing the fusion  
 CC polypeptide in the cell, and recovering the fusion polypeptide from the  
 CC host cell, optionally in the form of its salt; and (5) a vector for  
 CC expressing a polynucleotide sequence encoding a fusion polypeptide of  
 CC formula (I), (II), (III), (IV), or (V) or its salts (R<sub>1</sub>-L-R<sub>2</sub> (I), R<sub>2</sub>-  
 CC L-R<sub>1</sub> (II), R<sub>1</sub>-L-R<sub>2</sub>-L-R<sub>1</sub> (III), R<sub>1</sub>-L-R<sub>1</sub>-L-R<sub>2</sub> (IV), R<sub>2</sub>-L-R<sub>1</sub>-L-R<sub>1</sub>  
 CC (V), where R<sub>1</sub> = the polypeptide (a) or its truncation at the carboxy  
 CC terminus by 1-12 amino acids and R<sub>2</sub> = a polypeptide selected from the  
 CC sequence defined by residues Asp25-Leu609 the human HSA sequence  
 CC appearing as ABG32802, or its truncation at the carboxy terminus by 1-10  
 CC amino acids and L = independently a chemical bond, where the vector is  
 CC PWT3-Rla-HAS-Rla). The compositions and methods of the present invention  
 CC are useful for the prevention and treatment of systemic allergy and other  
 CC IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma  
 CC and chronic urticaria. The IgE-binding polypeptide have a more prolonged  
 CC effective serum life. The IgE-binding polypeptide have a more prolonged  
 CC effective clinical utility in the treatment of  
 CC allergy, as well as improved activity in a more efficient and cost-  
 CC effective manner. The present sequence is the human IgE receptor  
 CC FcpepsilonRIalpha used to make the fusion protein of the invention  
 XX Sequence 257 AA;

Query Match 100.0%; Score 1073; DB 5; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-77;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPNRRIFKGENVLTGNNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPNRRIFKGENVLTGNNFFEVS 60  
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 DB 61 STKWFHNGSLSEETNSSLNIVNAKFDGSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120  
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 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGALKYWEHNHNSITNATVEDSGTYCTGKV 180  
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 DB 181 WOLDYSEPLNITVIKA 197

RESULT 14  
 ABO01301  
 ID ABO01301\_standard; protein; 257 AA.  
 XX ABO01301;  
 AC ABO01301;  
 XX 07-AUG-2003 (first entry)  
 DT Human protein NOV8a.  
 XX Human; NOV8; cardiomyopathy; atherosclerosis; hypertension;  
 KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;  
 KW neoplasm; graft versus host disease; AIDS; bronchial asthma;  
 KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;  
 KW cancer-associated cachexia; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; immune disorder;  
 KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.

OS Homo sapiens.  
 XX WO2003023008-A2.  
 PN 20-MAR-2003.  
 XX 09-SEP-2002; 2002WO-US028596.  
 XX 07-SEP-2001; 2001US-0318120P.  
 PR 07-SEP-2001; 2001US-0318130P.  
 PR 10-SEP-2001; 2001US-0318430P.  
 PR 12-SEP-2001; 2001US-0318765P.  
 PR 17-SEP-2001; 2001US-0322781P.  
 PR 17-SEP-2001; 2001US-0322816P.  
 PR 19-SEP-2001; 2001US-0323519P.  
 PR 20-SEP-2001; 2001US-0323631P.  
 PR 20-SEP-2001; 2001US-0323636P.  
 PR 25-SEP-2001; 2001US-0324989P.  
 PR 25-SEP-2001; 2001US-0325091P.  
 PR 26-SEP-2001; 2001US-0324990P.  
 PR 15-FEB-2002; 2002US-0357303P.  
 PR 28-FEB-2002; 2002US-0360973P.  
 PR 28-MAR-2002; 2002US-0366131P.  
 PR 25-MAR-2002; 2002US-0367753P.  
 PR 02-APR-2002; 2002US-0369479P.  
 PR 10-MAY-2002; 2002US-0379532P.  
 PR 17-MAY-2002; 2002US-0381664P.  
 PR 17-MAY-2002; 2002US-0381672P.  
 PR 28-MAY-2002; 2002US-0383651P.  
 PR 29-MAY-2002; 2002US-0384012P.  
 PR 19-JUN-2002; 2002US-0390155P.  
 PR 06-SEP-2002; 2002US-00390155.  
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XX	RESULT 15
ADB85536	ADB85536 standard; protein; 257 AA.
AC AC	ADB85536;
DT	04-DEC-2003 (first entry)
DE DE	Human immunoglobulin E high affinity receptor alpha subunit protein.
KW KW	alpha subunit; high affinity receptor for immunoglobulin E; FCERI.
KW KW	mast cell; basophil; histamine; serotonin; allergic condition;
KW KW	antiallergic; allergic response; drug screening assay; immunoglobulin E;
XX XX	human.
CS CS	Homo sapiens.
FH FH	Key Location/Qualifiers
FT FT	Misc-difference 221 /note= "Encoded by GGA"
FT FT	Misc-difference 253 /note= "Encoded by AAC"
XX XX	US6602983-B1.
PV PV	OS-AUG-2003.
PD PD	22-SEP-1994; 94US-00310902.
PF PF	24-FEB-1988; 88US-00160457.
PR PR	30-OCT-1991; 91US-00785127.
PR PR	29-MAY-1993; 93US-00066640.
XX XX	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA PA	Kinet JP, Kochan JP;
XX XX	WPI; 2003-669612/63.
DR DR	N-PSDB; ADB85535.
XX XX	New alpha subunit of the human high affinity receptor for immunoglobulin
PT PT	E polypeptides, useful as antagonists to prevent allergic response, as
PT PT	reagents in drug screening assays, or for monitoring immunoglobulin E
XX XX	levels in patients.
PS PS	Claim 1; Fig 1; 9pp; English.
CC CC	This invention relates to a novel purified polypeptide corresponding to
CC CC	the alpha subunit of the human high affinity receptor for immunoglobulin
CC CC	E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC CC	invention is found exclusively on mast cells, basophils and related
CC CC	cells. Activation of the receptor triggers the release of preformed
CC CC	mediators such as histamine and serotonin which may result in allergic
CC CC	conditions. Compounds which modulate FcERI activity may have antiallergic
CC CC	activity. The polypeptide of the invention may be useful as an antagonist
CC CC	for preventing allergic response, as a reagent in drug screening assays,
CC CC	as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC CC	The DNA sequences may be useful for producing the polypeptide or for
CC CC	synthesising cDNA sequences to construct DNA probes used in diagnostic
CC CC	assays. The present sequence is the amino acid sequence of the alpha
CC CC	subunit of the human FcERI receptor of the invention.
XX XX	Sequence 257 AA;
SQ	
Query Match	100.0%; Score 1073; DB 7; Length 257;
Best Local Similarity	100.0%; Pred.No. 5.8e-77;
Matches 197; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 12.8578 Seconds  
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Title: US-10-763-400-11  
Perfect score: 1073  
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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1073	100.0	197	2	US-08-756-387B-11
2	1073	100.0	197	4	US-09-285-873-11
3	1073	100.0	197	4	US-09-944-277A-11
4	1073	100.0	257	1	US-07-869-933-11
5	1073	100.0	257	2	US-08-756-387B-2
6	1073	100.0	257	3	US-09-103-663-11
7	1073	100.0	257	4	US-09-285-873-2
8	1073	100.0	257	4	US-08-897-956A-1
9	1073	100.0	257	4	US-09-944-277A-2
10	1073	100.0	978	4	US-08-897-956A-3
11	1067	99.4	197	3	US-08-788-954-2
12	1032	96.2	193	2	US-08-756-387B-1
13	1032	96.2	193	5	PT-US93-08401-1
14	947	88.3	172	4	US-08-756-387B-13
15	947	88.3	172	4	US-09-285-873-13
16	947	88.3	172	4	US-08-245-764-9
17	947	88.3	172	4	US-09-944-277A-13
18	947	88.3	232	1	US-07-869-933-13
19	947	88.3	232	2	US-08-756-387B-6
20	947	88.3	232	3	US-08-103-663-13
21	947	88.3	232	4	US-09-285-873-6
22	947	88.3	232	4	US-09-944-277A-6
23	617	57.5	201	3	US-09-015-734-12
24	617	57.5	201	4	US-09-515-311-12
25	617	57.5	255	3	US-09-015-734-2
26	617	57.5	255	4	US-09-515-311-2
27	584	54.4	236	3	US-09-015-734-7

28	584	54.4	236	4	US-09-515-311-7	Sequence 7, Appli
29	554	51.6	199	3	US-08-833-488B-14	Sequence 14, Appl
30	545	50.8	197	3	US-08-833-488B-4	Sequence 4, Appli
31	545	50.8	197	3	US-08-833-488B-28	Sequence 28, Appl
32	545	50.8	253	3	US-08-833-488B-20	Sequence 20, Appl
33	543	50.6	197	3	US-08-833-488B-9	Sequence 9, Appli
34	538	50.1	431	4	US-09-592-998C-9	Sequence 9, Appli
35	538	50.1	435	4	US-09-592-998C-10	Sequence 10, Appl
36	522.5	48.7	199	2	US-08-768-964-12	Sequence 12, Appl
37	522.5	48.7	199	3	US-09-005-299-12	Sequence 12, Appl
38	522.5	48.7	199	3	US-09-515-431-12	Sequence 12, Appl
39	522.5	48.7	263	2	US-08-768-964-2	Sequence 2, Appli
40	522.5	48.7	263	3	US-09-005-299-2	Sequence 2, Appli
41	522.5	48.7	263	3	US-09-515-431-2	Sequence 2, Appli
42	516	48.1	173	3	US-08-833-488B-31	Sequence 31, Appl
43	516	48.1	229	3	US-08-833-488B-24	Sequence 24, Appl
44	491	45.8	174	2	US-08-768-964-13	Sequence 13, Appl
45	491	45.8	174	3	US-09-005-299-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-08-756-387B-11  
; Sequence 11, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-756-387B-11

Query Match 100.0%; Score 1073; DB 2; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
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Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120  
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Db 121 VMGQPLFLRCHGRWMDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
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Db 181 WOLDYSEPLNITVIKA 197

## RESULT 2

US-09-285-873-11  
; Sequence 11, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285, 873  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387  
; FILING DATE: No. 6309832ember 26, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
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; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-285-873-11

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Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
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; Sequence 11, Application US/09944277A  
; Patent No. 6682894  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944, 277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285, 873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-944-277A-11

Query Match 100.0%; Score 1073; DB 4; Length 197;  
Best Local Similarity 100.0%; Pred. No. 2.7e-98;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPNRIFKGNVTLTCGNFFEVS 60  
Db 1 MAPAMESPTLLCVALLFFAPDGVLPQPKVSLNPPNRIFKGNVTLTCGNFFEVS 60  
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120  
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLIQASAE 120  
QY 121 VMGQPLFLRCHGRWMDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
Db 121 VMGQPLFLRCHGRWMDVYKVIYYKDGEALKYWNHNISITNATVEDSGTYCTGKV 180  
QY 181 WOLDYSEPLNITVIKA 197

Db 181 WLDYSEPLNITVIKA 197

RESULT 4

US-07-869-933-11

Sequence 11, Application US/07869933

Patent No. 5770396

GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933

FILING DATE: 19920416

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/154 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-869-933-11

Query Match 100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 3.9e-98;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNFFVS 60

Db 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNFFVS 60

Qy 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

Db 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

Qy 121 VMWEGQPLFLCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180

Db 121 VMWEGQPLFLCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180

Qy 181 WLDYSEPLNITVIKA 197

Db 181 WLDYSEPLNITVIKA 197

RESULT 5

US-08-756-387B-2

Sequence 2, Application US/08756387B

Patent No. 5945294

GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.

APPLICANT: Rushlow, Keith E.

APPLICANT: Wassom, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hesk Corporation

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,387B

FILING DATE: No. 5945294ember 26, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-756-387B-2

Query Match 100.0%; Score 1073; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 3.9e-98;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNFFVS 60

Db 1 MAPAMESPTLLCVALLFPADGVLAVPQKPKVSLNPPNRRIFKGENVTLTCNGNFFVS 60

Qy 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

Db 61 STKWFHNGSLSEETNSSLNIVNAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLQASAE 120

Qy 121 VMWEGQPLFLCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180

Db 121 VMWEGQPLFLCHGRWMDVYKVIYKDGKALKYWEHNHISITNATVEDSGTYCTGKV 180

Qy 181 WLDYSEPLNITVIKA 197

Db 181 WLDYSEPLNITVIKA 197

RESULT 6

US-09-103-663-11

Sequence 11, Application US/09103663D

Patent No. 6171803

GENERAL INFORMATION:

APPLICANT: Kinet et al.

TITLE OF INVENTION: Isolation, characterization, and use of the human beta

TITLE OF INVENTION: subunit of the high affinity receptor for

TITLE OF INVENTION: immunoglobulin E.

FILE REFERENCE: 50490

CURRENT APPLICATION NUMBER: US/09/103,663D

CURRENT FILING DATE: 1998-06-23

EARLIER APPLICATION NUMBER: 07/869,933

EARLIER FILING DATE: 1992-04-16

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 11
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-11

Query Match      100.0%; Score 1073; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 7
US-09-285-873-2
; Sequence 2, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassow, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-2

Query Match      100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 8
US-08-897-956A-1
; Sequence 1, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-08-897-956A-1

Query Match      100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
Db 1 MAPAMESPTLLCVALLFFAPDGVLA VPKPKVSLNPPNRI FKGNVTLTCNGNFFEVS 60
QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
Db 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCOHQVNESEPVVLEFVSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
Db 121 VMGQPLFLRCHGWRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
Db 181 WLDYSEPLNITVIKA 197

RESULT 9
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. 6682894
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassow, Donald L.
```

Tue Oct 12 09:19:21 2004

```
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

Query Match 100.0%; Score 1073; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.9e-98;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
QY 121 VMMEGQPLFLRCHGWRWDVYKVIYYKDGEALKYWNHNHISITNATVEDSGTYCTGKV 180
DB 121 VMMEGQPLFLRCHGWRWDVYKVIYYKDGEALKYWNHNHISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
DB 181 WLDYSEPLNITVIKA 197

RESULT 10
US-08-897-956A-3
; Sequence 3, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26

; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 978
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-08-897-956A-3

Query Match 100.0%; Score 1073; DB 4; Length 978;
Best Local Similarity 100.0%; Pred. No. 2.5e-97;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
DB 1 MAPAMESPTLLCVALLFFAPDGLAVPQPKVSLNPPWNRIFKGENVTLFCNGNPFVS 60
QY 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
QY 121 VMMEGQPLFLRCHGWRWDVYKVIYYKDGEALKYWNHNHISITNATVEDSGTYCTGKV 180
DB 121 VMMEGQPLFLRCHGWRWDVYKVIYYKDGEALKYWNHNHISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
DB 181 WLDYSEPLNITVIKA 197

RESULT 11
US-08-788-954-2
; Sequence 2, Application US/08788954
; Patent No. 6090384
; GENERAL INFORMATION:
; APPLICANT: RA, CHISEI
; APPLICANT: NAITO, KOJI
; APPLICANT: HIRAWA, MINORU
; APPLICANT: OKUMURA, KO
; TITLE OF INVENTION: ANTIALLERGIC COMPOSITION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SUGHRUB, MION, ZINN, MACPEAK, & SEAS
; STREET: 2100 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,954
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,188
; FILING DATE:
; APPLICATION NUMBER: US 08/023,912
; FILING DATE: 26-FEB-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-788-954-2

Query Match 99.4%; Score 1067; DB 3; Length 197;  
 Best Local Similarity 99.5%; Pred. No. 1.1e-97;  
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLCNGNNFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFPADGVLAVPQPKVFLNPPNRRIFKGENVTLCNGNNFFEVS 60  
 QY 61 STKWFHNSLSSETSSLNINAKFEDSGEYKCOHQVNESEPVYLVFSDWLLLOASAE 120  
 DB 61 STKWFHNSLSSETSSLNINAKFEDSGEYKCOHQVNESEPVYLVFSDWLLLOASAE 120  
 QY 121 VMEGQPLFLRCHGWRNDVYKVIYYKDGEALKWYENHNISITNATVEDSGTYCTGKV 180  
 DB 121 VMEGQPLFLRCHGWRNDVYKVIYYKDGEALKWYENHNISITNATVEDSGTYCTGKV 180  
 QY 181 WLDYSEPLNITVIKA 197  
 DB 181 WLDYSEPLNITVIKA 197

RESULT 12

US-08-765-536-1

; Sequence 1, Application US/08765536

; Patent No. 5962634

; GENERAL INFORMATION:

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Sutton, Brian J.

; APPLICANT: McDonnell, James M.

; APPLICANT: Gould, Hannah J.

; APPLICANT: Korngold, Robert

; APPLICANT: Beavil, Andrew J.

; TITLE OF INVENTION: Ige Antagonists

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &amp; No. 5962634ris

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,536

; FILING DATE: April 30, 1997

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,943

; FILING DATE: 08-JUL-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TCU-1619

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-765-536-1

Query Match 96.2%; Score 1032; DB 2; Length 193;  
 Best Local Similarity 99.0%; Pred. No. 3e-94;  
 Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLCNGNNFFEVSSTKWF 65  
 DB 1 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLCNGNNFFEVSSTKWF 60  
 QY 66 HNGSLSEETSSLNINAKFEDSGEYKCOHQVNESEPVYLVFSDWLLLOASAEVWMEG 125  
 DB 61 HNGSLSEETSSLNINAKFEDSGEYKCOHQVNESEPVYLVFSDWLLLOASAEVWMEG 120  
 QY 126 QPLFLRCHGWRNDVYKVIYYKDGEALKWYENHNISITNATVEDSGTYCTGKVWQLDY 185  
 DB 121 QPLFLRCHGWRNDVYKVIYYKDGEALKWYENHNISITNATVEDSGTYCTGKVWQLDY 180  
 QY 186 ESEPLNITVIKA 197  
 DB 181 ESEPLNITVIKA 192

RESULT 13

PCT-US95-08401-1

; Sequence 1, Application PC/TUS9508401

; GENERAL INFORMATION:

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Sutton, Brian J.

; APPLICANT: McDonnell, James M.

; APPLICANT: Gould, Hannah J.

; APPLICANT: Korngold, Robert

; APPLICANT: Beavil, Andrew J.

; TITLE OF INVENTION: Ige Antagonists

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &amp;

; STREET: One Liberty Place, 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08401

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,943

; FILING DATE: 08-JUL-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Deluca, Mark

; REGISTRATION NUMBER: 33,229

; REFERENCE/DOCKET NUMBER: TCU-1597

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 193 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-08401-1

Query Match 96.2%; Score 1032; DB 5; Length 193;  
 Best Local Similarity 99.0%; Pred. No. 3e-94;  
 Matches 190; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLCNGNNFFEVSSTKWF 65  
 DB 1 ESTTLCVALLFPADGVLAVPQPKVSLNPPNRRIFKGENVTLCNGNNFFEVSSTKWF 60



Db 1 ESEPLNITVKA 197  
QY 66 HNSLSEETNSSLNINAKFEDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEG 125  
Db 61 HNSLSEETNSSLNINAKFEDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEG 120  
QY 126 QPLFLCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDY 185  
Db 121 QPLFLCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDY 180  
QY 186 ESEPLNITVKA 197  
Db 181 ESEPLNITVKA 192

RESULT 14  
US-08-756-387B-13  
; Sequence 13, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Haska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/756,387B  
; APPLICATION NUMBER: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 172 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-756-387B-13

Query Match 88.3%; Score 947; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 6.3e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 VPQPKVSLNPPWNRIFKGENVTLCNGNFFEVSSSTKWFHNGSLSEETNSSLNINAKF 60  
QY 86 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNDVYKVIY 145  
Db 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNDVYKVIY 120  
QY 146 YKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDYSEPLNITVKA 197  
Db 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDYSEPLNITVKA 172

Search completed: October 6, 2004, 09:04:38  
Job time : 13.8578 secs

RESULT 15  
US-09-285-873-13  
; Sequence 13, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Haska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Wordperfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,873  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387  
; FILING DATE: No. 6309832ember 26, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 172 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-285-873-13

Query Match 88.3%; Score 947; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 6.3e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 VPQPKVSLNPPWNRIFKGENVTLCNGNFFEVSSSTKWFHNGSLSEETNSSLNINAKF 85  
Db 1 VPQPKVSLNPPWNRIFKGENVTLCNGNFFEVSSSTKWFHNGSLSEETNSSLNINAKF 60  
QY 86 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNDVYKVIY 145  
Db 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVWMEGQPLFLRCHGWRNDVYKVIY 120  
QY 146 YKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDYSEPLNITVKA 197  
Db 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKWKWQLDYSEPLNITVKA 172

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Sequence 9, Appli  
Sequence 23, Appli  
Sequence 10, Appli  
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Sequence 30, Appli  
Sequence 14, Appli  
Sequence 65, Appli  
Sequence 117, Appli  
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ALIGNMENTS

RESULT 1  
US-09-944-277A-11  
; Sequence 11, Application US/09944277A  
; Patent No. US20020034771A1  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
Porter, James P.  
Rushlow, Keith E.  
Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/464-9505

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	9	US-09-944-277A-11
2	1073	100.0	257	9	US-09-944-277A-2
3	1073	100.0	257	12	US-10-236-392-28
4	1073	100.0	257	14	US-10-384-850-45
5	947	88.3	172	9	US-09-944-277A-13
6	947	88.3	172	9	US-09-245-764-9
7	947	88.3	172	12	US-10-293-992-4
8	947	88.3	172	12	US-10-687-109-9
9	947	88.3	176	10	US-09-809-715-2
10	947	88.3	176	12	US-10-293-992-2
11	947	88.3	232	9	US-09-944-277A-6
12	922	85.9	176	10	US-09-809-715-4
13	840.5	78.3	218	12	US-10-236-392-30
14	617	57.5	201	15	US-10-434-817-12
15	617	57.5	255	15	US-10-434-817-2

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 60.1562 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-10-763-400-11  
Perfect score: 1073  
Sequence: 1 MAPAMESPLLCVALLFPAP.....GKVMQDYSEBPNITVIKA 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
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  - 2: /cgn2\_6/prodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/prodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 5: /cgn2\_6/prodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
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  - 15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

Query Match          100.0%; Score 1073; DB 9; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.4e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
DB 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGRWMDVKVIYKDGKALKYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGQPLFLRCHGRWMDVKVIYKDGKALKYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
DB 181 WLDYSEPLNITVIKA 197

RESULT 2
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Forster, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <UNKNOWN>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,453
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

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Best Local Similarity 100.0%; Pred. No. 3.3e-86;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 STKWFHNGSLSEETNSSLNINAKPEDSGEYKCOHQVNESEPVYLEVFSDWLLLOASAE 120
QY 121 VMGQPLFLRCHGRWMDVKVIYKDGKALKYENHNISITNATVEDSGTYCTGKV 180
DB 121 VMGQPLFLRCHGRWMDVKVIYKDGKALKYENHNISITNATVEDSGTYCTGKV 180
QY 181 WLDYSEPLNITVIKA 197
DB 181 WLDYSEPLNITVIKA 197

RESULT 3
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, Li, Li
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Smithson, Richard A
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
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; PRIOR FILING DATE: 2002-02-15  
 ; PRIOR APPLICATION NUMBER: US60/367,753  
 ; PRIOR FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER: US60/369,479  
 ; PRIOR FILING DATE: 2002-04-02  
 ; PRIOR APPLICATION NUMBER: US09/659,634  
 ; PRIOR FILING DATE: 2000-09-12  
 ; PRIOR APPLICATION NUMBER: US60/318,120  
 ; PRIOR FILING DATE: 2001-09-07  
 ; PRIOR APPLICATION NUMBER: US60/318,130  
 ; PRIOR FILING DATE: 2001-09-07  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 794  
 ; SOFTWARE: Custom  
 ; LENGTH: 257  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-384-850-45

Query Match 100.0%; Score 1073; DB 12; Length 257;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MAPAMESPTLLCVALFPAPDGLAVPQPKVSLNPPNRIKFGENTVLTGNGNPFVS 60  
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 QY 181 WOLDYSEPLNITVIKA 197  
 DB 181 WOLDYSEPLNITVIKA 197

RESULT 4  
 US-10-384-850-45  
 ; Sequence 45, Application US/10384850  
 ; Publication No. US20030175890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: C. Fraser  
 ; TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF  
 ; FILE REFERENCE: 7853-217  
 ; CURRENT APPLICATION NUMBER: US/10/384,850  
 ; CURRENT FILING DATE: 2003-03-10  
 ; PRIOR APPLICATION NUMBER: US/09/702,021  
 ; PRIOR FILING DATE: 2000-10-30  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 45  
 ; LENGTH: 257  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-384-850-45

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 DB 181 WOLDYSEPLNITVIKA 197

RESULT 5

US-09-944-277A-13  
 ; Sequence 13, Application US/09944277A  
 ; Patent No. US20020034771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank, Glenn R.  
 ; Porter, James P.  
 ; Rushlow, Keith E.  
 ; Hassom, Donald L.

TITLE OF INVENTION: Method to Detect IgE  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Carol Talkington Verser, Ph.D.  
 Heeka Corporation  
 STREET: 1825 Sharp Point Drive  
 CITY: Fort Collins  
 STATE: Colorado  
 COUNTRY: USA  
 ZIP: 80525

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WordPerfect for Windows, Version 7.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/944,277A  
 FILING DATE: 30-Aug-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/285,873  
 FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:  
 NAME: Verser, Carol Talkington  
 REGISTRATION NUMBER: 37,459  
 REFERENCE/DOCKET NUMBER: DI-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 970/493-7272  
 TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 172 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-944-277A-13

Query Match 88.3%; Score 947; DB 9; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPQPKVSLNPPNRIKFGENTVLTGNGNPFVSSTKWFHNGSLSEETNSLNINAKF 85  
 DB 1 VPQPKVSLNPPNRIKFGENTVLTGNGNPFVSSTKWFHNGSLSEETNSLNINAKF 60  
 QY 86 EDSGEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMESQPLFLRCHGRNWDVYKVIY 145  
 DB 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQASAEVVMESQPLFLRCHGRNWDVYKVIY 120  
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FILE REFERENCE: AL-8  
; CURRENT APPLICATION NUMBER: US/09/809,715  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,853  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-715-2

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RESULT 10  
US-10-293-992-2  
; Sequence 2, Application US/10293992  
; Publication No. US20040033527A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Kinet, Jean-Pierre  
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR  
; FILE REFERENCE: AL-3-C1-1  
; CURRENT APPLICATION NUMBER: US/10/293,992  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/434,193  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,219  
; PRIOR FILING DATE: 1998-11-05  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-992-2

Query Match 88.3%; Score 947; DB 12; Length 176;  
Best Local Similarity 100.0%; Pred. No. 2.5e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPOKPKVSLNPPWNRIFKGENVTILTCGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85  
Db 1 VPOKPKVSLNPPWNRIFKGENVTILTCGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145  
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 146 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKA 197  
Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKA 172

RESULT 11

US-09-944-277A-6  
; Sequence 6, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-944-277A-6

Query Match 88.3%; Score 947; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 3.5e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VPOKPKVSLNPPWNRIFKGENVTILTCGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 85  
Db 1 VPOKPKVSLNPPWNRIFKGENVTILTCGNFFVSVSTKWFHNGSLSEETNSSLNINAKF 60

QY 86 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145  
Db 61 EDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 146 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKA 197  
Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITVIKA 172

RESULT 12  
US-09-809-715-4  
; Sequence 4, Application US/09809715  
; Publication No. US20030003502A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtetzky, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Wurzburg, Beth A.  
; APPLICANT: Kinet, Jean-Pierre  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC





CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,734  
FILING DATE: 29-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 201 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-434-817-12

Query Match 57.5%; Score 617; DB 15; Length 201;  
Best Local Similarity 60.2%; Pred. No. 3e-46;  
Matches 121; Conservative 24; Mismatches 52; Indels 4; Gaps 1;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLCNGNPFVEVS 60  
DB 1 MPAPMGSPALLWITFLFSLDGVPAAIRKSTVSLNPPNRIFRGENVTLCNKNKPLKGN 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQOVNESEPVYLEVFSDDLLOASAE 120  
DB 61 STEWTYNTTLEVTTSLSNITNASHRSSEYRCRNNDNLSEAVHLEVFSDWLLLOASAE 120

QY 121 VMGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG-- 178  
DB 121 EVIEGKALVLRCKGKWDVFKVIYKDGKPLEYWKYENKNISIESATENSGETTYCEGAF 180

QY 179 --KVMQLDYSESEPLNITVIKA 197  
DB 181 NFKRTSERYTSDYLNITVKKA 201

RESULT 15  
US-10-434-817-2  
Sequence 2, Application US/10434817  
Publication No. US20030235579A1  
GENERAL INFORMATION:  
APPLICANT: Weber, Eric R.  
TITLE OF INVENTION: NOVEL EQUINE PC EPSILON RECEPTOR ALPHA  
CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heskia Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/434,817  
FILING DATE: 08-May-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,734  
FILING DATE: 29-JAN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 255 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-434-817-2

Query Match 57.5%; Score 617; DB 15; Length 255;  
Best Local Similarity 60.2%; Pred. No. 3.9e-46;  
Matches 121; Conservative 24; Mismatches 52; Indels 4; Gaps 1;

QY 1 MAPAMESPTLLCVALLFFAPDGVLAVPQPKVSLNPPNRIFKGENVTLCNGNPFVEVS 60  
DB 1 MPAPMGSPALLWITFLFSLDGVPAAIRKSTVSLNPPNRIFRGENVTLCNKNKPLKGN 60

QY 61 STKWFHNGSLSEETNSLNIIVNAKFEDSGEYKCOHQOVNESEPVYLEVFSDDLLOASAE 120  
DB 61 STEWTYNTTLEVTTSLSNITNASHRSSEYRCRNNDNLSEAVHLEVFSDWLLLOASAE 120

QY 121 VMGQPLFLRCHGRNWDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG-- 178  
DB 121 EVIEGKALVLRCKGKWDVFKVIYKDGKPLEYWKYENKNISIESATENSGETTYCEGAF 180

QY 179 --KVMQLDYSESEPLNITVIKA 197  
DB 181 NFKRTSERYTSDYLNITVKKA 201

Search completed: October 6, 2004, 09:28:10  
Job time : 60.1562 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 10.7914 Seconds  
(without alignments)  
1756.007 Million cell updates/sec

Title: US-10-763-400-11  
Perfect score: 1073  
Sequence: 1 MAPAMESPTLLCVALLFPAP.....GKVMQLDYESBPLNITVIKA 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1073	100.0	257	2	S00682
2	511	47.6	250	2	A34342
3	489	45.6	245	2	A30154
4	405	37.7	296	2	I46021
5	386.5	36.0	270	2	A34636
6	373	35.3	404	2	A46480
7	376	35.0	344	2	A41357
8	376	35.0	374	1	A39878
9	375.5	35.0	280	2	I55577
10	373.5	34.8	336	2	I48471
11	367.5	34.2	254	1	JL0107
12	366	34.1	261	2	S29360
13	364.5	34.0	285	2	S36903
14	363.5	33.9	233	1	JU0284
15	362	33.7	267	2	I56110
16	361.5	33.7	323	2	S06946
17	358	33.4	267	2	A35902
18	357.5	33.3	283	1	FCMSG1
19	357.5	33.3	310	2	JL0119
20	357.5	33.3	330	2	A40071
21	357.5	33.3	330	2	I49660
22	348	32.4	157	2	D31327
23	347	32.3	317	2	JL0118
24	343	32.0	267	2	I72882
25	338	31.5	160	2	I47163
26	220	20.5	159	2	I47164
27	184.5	15.3	1694	2	S50065
28	156	14.5	104	2	I47165
29	136.5	12.7	458	1	MMMSK1

30 136.5 12.7 458 2 JCL1509  
31 136.5 12.7 521 2 JCL1508  
32 136.5 12.7 521 2 S34338  
33 132 12.3 7962 2 I38346  
34 130 12.1 458 2 S23969  
35 130 12.1 458 2 S68177  
36 130 12.1 519 2 A44783  
37 129.5 12.1 344 2 A27681  
38 127 11.8 538 2 JCL2457  
39 126.5 11.8 1239 1 A32579  
40 126 11.7 1327 2 T09402  
41 125.5 11.7 978 2 S16385  
42 123.5 11.5 264 2 I46020  
43 123.5 11.5 976 1 TVMSMD  
44 120 11.2 702 2 A36319  
45 120 11.2 6642 2 T29757

#### ALIGNMENTS

##### RESULT 1

S00682  
Igf Fc receptor alpha chain precursor - human  
N/Alternate names: Fc-epsilon receptor  
C/Species: Homo sapiens (man)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 23-Jul-1999  
C/Accession: S00682; B30154; S42209  
R/Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.  
Nucleic Acids Res. 16, 3584, 1988  
A/Title: Isolation of the gene coding for the alpha subunit of the human high affinity )  
A/Reference number: S00682; MUID:88233953; PMID:2967464  
A/Accession: S00682  
A/Molecule type: mRNA  
A/Residues: 1-257 <KOC>  
A/Cross-references: ENBL:X06948; NID:g31317; PIDN:CAA30025.1; PID:g31318  
R/Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
A/Title: Human and rat mast cell high-affinity immunoglobulin E receptors: Characterizat  
A/Reference number: A34191; MUID:88158102; PMID:2964640  
A/Accession: B30154  
A/Molecule type: mRNA  
A/Residues: 1-257 <SHI>  
A/Cross-references: J03605; NID:g187449; PIDN:AAA36204.1; PID:g307164  
R/Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.  
Eur. J. Biochem. 220, 593-598, 1994  
A/Title: High-level expression of the truncated alpha chain of human high-affinity recei  
nant product.  
A/Reference number: S42209; MUID:94170811; PMID:8125119  
A/Accession: S42209  
A/Molecule type: protein  
A/Residues: 26-197 <YAG>  
A/Experimental source: Purified recombinant protein  
C/Genetics:  
A/Gene: GDB:FCER1A  
A/Cross-references: GDB:119902; OMIM:147140  
A/Map position: Iq23-Iq23  
C/Supfamily: Fc gamma receptor III; immunoglobulin homology  
C/Keywords: immunoglobulin receptor; transmembrane protein  
F/1-25/Domain: signal sequence #status predicted <SIG>  
F/26-257/Product: IgE Fc receptor alpha chain #status predicted <MAT>  
F/44-95/Domain: immunoglobulin homology <IMM1>  
F/125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 1073; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.5e-78;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPAMESPTLLCVALLFPAPDGVAVPQPKVSLPPNRRIFKGNVTLTCNNFFEVS 60

Db 1 MAPAMESPTLLCVALLFPAPDGVAVPQPKVSLPPNRRIFKGNVTLTCNNFFEVS 60

QY 61 STKWFHNGSLSETNSLNINAKTFDSGEYKQCQVNESEPVYLEVFSDWLLIQAAS 120

Db 61 STKWFHNSLSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLVFSDMLLQASAE 120  
QY 121 VVMEQPLFLRCHGRNWDVVKVYIKDGEALKYWHENHNSITNATVEDSGTYCTGKV 180  
Db 121 VVMEQPLFLRCHGRNWDVVKVYIKDGEALKYWHENHNSITNATVEDSGTYCTGKV 180  
QY 181 WOLDYESPLNITVIKA 197  
Db 181 WOLDYESPLNITVIKA 197

## RESULT 2

A34342  
Igc Fc receptor alpha chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 23-Jul-1999  
C:Accession: A34342; A61238  
R:Ra, C.; Jouvin, M.H.E.; Kinet, J.P.  
J. Biol. Chem. 264, 15323-15327, 1989  
A:Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and  
A:Reference number: A34342; MUID:89359361; PMID:2527850  
A:Accession: A34342  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-250 <RAC>  
A:Cross-references: GB:J05018; NID:G193236; PIDN:AAA37600.1; PID:G309224  
R:Robertson, M.W.; Menl, V.S.; Richards, M.L.; Liu, F.T.  
Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991  
A:Title: mRNA variants encoding multiple forms of the high-affinity IgE receptor alpha s  
A:Reference number: A61238; MUID:92234569; PMID:1839735  
A:Accession: A61238  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 125-194 <ROB>  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein  
F:42-94/Domain: immunoglobulin homology <IMM>

Query Match 47.6%; Score 511; DB 2; Length 250;  
Best Local Similarity 51.1%; Pred. No. 1.1e-33;  
Matches 96; Conservative 38; Mismatches 52; Indels 2; Gaps 2;  
QY 11 LCVALFPAPDGVLAVPQKPVSLNPPNRRIFKGNVTLTCNGNPFV-SSTKWFHNS 69  
Db 9 LCLALLFMSLDVILTATEKSVLTLDPPWIRIFTGKVTLSYGNHLMQNSTTKWIHNGT 68  
QY 70 LSEETNSSLNINAKFDSGEYKCOHQVNESEPVYLVFSDMLLQASAEVWMEQPLFL 129  
Db 69 VSEVNSSHLVTSATVQDSGKYTCQKGLFKSPVYLVNTQDMLLQTSADMLVHGSFD 128  
QY 130 LRCHGRNWDVVKVYIKDGEALKYWHENHNSITNATVEDSGTYCTGKVWOLDYESEP 189  
Db 129 IRCHGRNWDVVKVYIYNDHAFNYSVES-PVSIREATLNDSTGYHCKGVLQVQVESDK 187  
QY 190 LNITVIKA 197  
Db 188 FRIAWVKA 195

## RESULT 3

A30154  
Igc receptor alpha chain precursor - rat  
N:Alternate names: Fc-epsilon-R alpha chain precursor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 21-Jan-2000  
C:Accession: C31327; A31327; A30154; A27116; I55304  
R:Liu, F.T.; Albrandt, K.; Robertson, M.W.  
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988  
A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ig  
A:Reference number: A94203; MUID:88289772; PMID:2969594  
A:Accession: C31327  
A:Molecule type: mRNA

A:Residues: 1-245 <LIU>  
A:Cross-references: GB:M21622; GB:J03811  
A:Experimental source: basophilic leukemia cell line, clone R3-4  
A:Accession: A31327  
A:Molecule type: mRNA  
A:Residues: 21-245 <LI3>  
A:Cross-references: GB:M21622; NID:G204109; PIDN:AAA41146.1; PID:G204110; GB:J03811  
A:Experimental source: basophilic leukemia cell line  
R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterization  
A:Reference number: A94191; MUID:88158102; PMID:2964640  
A:Accession: A30154  
A:Molecule type: mRNA  
A:Residues: 1-245 <SHI>  
A:Cross-references: GB:J03606; NID:G205331; PIDN:AAA41582.1; PID:G205332  
R:Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.  
Biochemistry 26, 4605-4610, 1987  
A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff  
A:Reference number: A27116; MUID:88024987; PMID:2959318  
A:Accession: A27116  
A:Molecule type: mRNA  
A:Residues: 1, 'G', '3-236', 'N', '238-244', 'RLKPNs', <KIN>  
R:Tepler, I.; Shimizu, A.; Leder, P.  
J. Biol. Chem. 264, 5912-5915, 1989  
A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structural  
A:Reference number: I55304; MUID:89174653; PMID:2522441  
A:Accession: I55304  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-16 <RES>  
A:Cross-references: GB:M25334; NID:G341335; PIDN:AAA74562.1; PID:G556391  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: immunoglobulin receptor; transmembrane protein  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>  
F:42-93/Domain: immunoglobulin homology <IMM>

Query Match 45.6%; Score 489; DB 2; Length 245;  
Best Local Similarity 48.9%; Pred. No. 6.2e-32;  
Matches 91; Conservative 37; Mismatches 56; Indels 0; Gaps 0;  
QY 11 LCVALFPAPDGVLAVPQKPVSLNPPNRRIFKGNVTLTCNGNPFV-SSTKWFHNSL 70  
Db 9 LCLALLFSLGWLTAQKSVVSLDPPWIRILTGDVTLICNGNNSQMSNTKWIHNDI 68  
QY 71 SEETNSSLNINAKFDSGEYKCOHQVNESEPVYLVFSDMLLQASAEVWMEQPLFL 130  
Db 69 SNVXSSHWIVTSATVQDSGKYTCQKGLFKSPVYLVNTQDMLLQTSADMLVHGSFDI 128  
QY 131 RCHGRNWDVVKVYIKDGEALKYWHENHNSITNATVEDSGTYCTGKVWOLDYESEP 190  
Db 129 RCRSKKKVHKVYIKDDIAFKYSYDSNNTSIRKAFNDSGSYHCTGYLNKVECKSDKF 188  
QY 191 NITVIK 196  
Db 189 SIAYVK 194  
RESULT 4  
I46021  
Fc-gamma receptor II - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 23-Jul-1999  
C:Accession: I46021; S40204  
R:Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.  
Immunogenetics 39, 423-427, 1994  
A:Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.  
A:Reference number: I46021; MUID:94245284; PMID:8188320  
A:Accession: I46021  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-296 <ZHA>

J. Immunol. 148, 1570-1575, 1992  
A>Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and  
A/Reference number: A46480; MUID:92166399; PMID:1531670  
A/Accession: A46480  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-404 <OSM>  
A/Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC  
R/Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.  
J. Immunol. 144, 371-378, 1990  
A>Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG  
A/Reference number: A43511; MUID:90111035; PMID:2136886  
A/Accession: A43511  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-404 <SEA>  
A/Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753  
C/Superfamily: Fc gamma receptor I; immunoglobulin homology  
C/Keywords: immunoglobulin receptor; transmembrane protein  
F:127-179/Domain: immunoglobulin homology <IMM>

Query Match 35.3%; Score 379; DB 2; Length 404;  
Best Local Similarity 41.6%; Pred. No. 6.7e-23;  
Matches 77; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

QY 10 LLCVALLFPADGVAVPQPKVSLNPPNRIKGENVTLTCGNPFVSVSTKWFHNGS 69  
Db 12 LLTLLLVVPVGVNATKAVITLQPPWISIFOKENVTLWCEGHLPDGDSTQWFI NGT 71  
QY 70 LSEETNSLNTVNAKFDSGEYKQHQVNESEPVYLEVFSDDLILQASAEVVMGQPLF 129  
Db 72 AVQISTPSYSIPESAFQDSGEYRCQIGSSMPSPDVLQIHNHDLWLLQASRRVLTEGEPLA 131  
QY 130 LRCHGWRNDVYKVIYKDGALKYVENHNISITNATVEDSGTYCTCKVQWLDYSESE 189  
Db 132 LRCHGWRNDVYKVIYKDGALKYVENHNISITNATVEDSGTYCTCKVQWLDYSESE 189  
QY 190 LNIIV 194  
Db 190 VSIIV 194

RESULT 7  
A41357  
Fc gamma (IgG) receptor I (high affinity) form b - human  
N/Alternate names: CD84  
C/Species: Homo sapiens (man)  
C/Date: 03-Apr-1992 #sequence\_revision 03-Apr-1992 #text\_change 21-Jan-2000  
C/Accession: A41357; S03019  
R/Allen, J.M.; Seed, B.  
Science 243, 378-381, 1989  
A/Title: Isolation and expression of functional high-affinity Fc receptor complementary  
A/Reference number: A41357; MUID:89100284; PMID:2911749  
A/Accession: A41357  
A/Molecule type: mRNA  
A/Residues: 1-344 <ALL1>  
A/Cross-references: GB:X14355; GB:M21090; NID:g31333; PIDN:CAA32536.1; PID:g31334  
R/Allen, J.M.; Seed, B.  
Nucleic Acids Res. 16, 11824, 1988  
A/Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (Fc  
A/Reference number: S03018; MUID:89098339; PMID:2974947  
A/Accession: S03019  
A/Molecule type: mRNA  
A/Residues: 1-344 <ALL2>  
A/Cross-references: EMBL:X14355; NID:g31333; PIDN:CAA32536.1; PID:g31334  
A/Note: the authors translated the codon ACT for residue 25 as Ala  
C/Superfamily: Fc gamma receptor I; immunoglobulin homology  
C/Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein  
F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 35.0%; Score 376; DB 2; Length 344;  
Best Local Similarity 39.7%; Pred. No. 9.7e-23;  
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

A/Cross-references: EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g437979  
A/Superfamily: Fc gamma receptor III; immunoglobulin homology  
C/Keywords: immunoglobulin receptor

Query Match 37.7%; Score 405; DB 2; Length 296;  
Best Local Similarity 42.2%; Pred. No. 3.9e-25;  
Matches 79; Conservative 33; Mismatches 71; Indels 4; Gaps 2;

QY 10 LLCVALLFPADGVAVPQPKVSLNPPNRIKGENVTLTCGNPFVSVSTKWFHNGS 67  
Db 29 LLTALLFLAP--VSGKPLPKAVVTIQPAWNLVREDHVTTCQGTSPSAGNLTTFWPHN 86  
QY 68 GLSSEETNSLNTVNAKFDSGEYKQHQVNESEPVYLEVFSDDLILQASAEVVMGQPL 127  
Db 87 GSIHTQKQPSYFRAGSNDGSGYRCQREOTSLSDPVLVDVSDWLLQTPSLVFPQEGEP 146  
QY 128 LFRCHGWRNDVYKVIYKDGALKYVENHNISITNATVEDSGTYCTCKVQWLDYSESE 187  
Db 147 IMLRCHSWRNOPLNKITFYQDRSKISFYQRTNFSIPRANLSHSGQYHCTAFIGKMLHSS 206  
QY 188 EPLNITV 194  
Db 207 QPNITV 213

RESULT 5  
A34636  
Fc gamma receptor II precursor - guinea pig  
C/Species: Cavia porcellus (guinea pig)  
C/Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 16-Jul-1999  
C/Accession: A34636  
R/Tominaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.  
Biochem. Biophys. Res. Commun. 168, 683-689, 1990  
A/Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (H  
A/Reference number: A34636; MUID:90241239; PMID:1692213  
A/Accession: A34636  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-270 <TOM>  
A/Cross-references: GB:M35272  
C/Superfamily: Fc gamma receptor III; immunoglobulin homology  
C/Keywords: immunoglobulin receptor  
F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 36.0%; Score 386.5; DB 2; Length 270;  
Best Local Similarity 43.5%; Pred. No. 1.1e-23;  
Matches 81; Conservative 23; Mismatches 81; Indels 1; Gaps 1;

QY 10 LLCVALLFPAP--DGVAVPQPKVSLNPPNRIKGENVTLTCGNPFVSVSTKWFHNG 68  
Db 2 LLTITVFLAPVAGTSADPPKAVVRLEPPWIVQVLRGDRVLTCEGAPSPGNHSTQWLHNG 61  
QY 69 SLSEETNSLNTVNAKFDSGEYKQHQVNESEPVYLEVFSDDLILQASAEVVMGQPL 128  
Db 62 RLITQVLPVSRFTAKGNDGSGYRCQAGTSLSDPVLVDVSDWLLVLTQSLIFQEGDVI 121  
QY 129 FLRCHGWRNDVYKVIYKDGALKYVENHNISITNATVEDSGTYCTCKVQWLDYSESE 198  
Db 122 VLRSCHSWNPLAKVTYTHNGVAKKYFSISKNFSPQANHSHSGAYNCTLGRTGHTSP 181  
QY 189 PLNITV 194  
Db 182 PVTITV 187

RESULT 6  
A46480  
Fc gamma (IgG) receptor high affinity - mouse  
N/Alternate names: high affinity IgG receptor  
C/Species: Mus musculus (house mouse)  
C/Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: A46480; A43511  
R/Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.

C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane F;1-15/Domain: signal sequence #status predicted <SIG>  
F;16-292/Domain: extracellular #status predicted <EXT>  
F;117-170/Domain: immunoglobulin homology <IMM2>  
F;293-313/Domain: transmembrane #status predicted <TMW>  
F;59,78,152,159,163,195,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 376; DB 1; Length 374;  
Best Local Similarity 39.7%; Pred. No. 1.le-22;  
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVTLTCGNNFFVSVSTKWFHNGSL 70  
DB 4 LITLLLVWVVDGQVDT-KKAVITLQPPWVSFQEEVTILHCEVLHLPQSSSTQWFLNGTA 62

QY 71 SEETNSLNIIVNAKFDSEGEYKCOHQOVNESPVLYLEFSDWLLLOQASAEVVMGQPLFL 130  
DB 63 TOTSTPSYRITASVNDSEYRCQGLSGRSDPIQLEIHRGWLMLLOQVSRVFMGEPLAL 122

QY 131 RCHGWRNDVYKVIYKDGKALKYVNNENISINATVEDSGTYTCGKVMOLDYSEPL 190  
DB 123 RCHAWKKLVNVIYTRNGKAPFPWNSLILKTNISHNGTYHCSG-MGKHRYTSAGI 181

QY 191 NITV 194  
DB 182 SVTV 185

RESULT 9  
Fc gamma (IG) receptor I-B splice form 1 precursor - human  
N;Alternate names: CD64  
N;Contains: Fc-gamma (IG) receptor I-B splice form 2  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
C;Accession: I55577; I70303  
R;Porges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.  
J. Clin. Invest. 90, 2102-2109, 1992  
A;Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.  
A;Reference number: I55577; MUID:93055454; PMID:1430234  
A;Accession: I55577  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-280 <RES>  
A;Cross-references: GB:I03419; NID:g182460; PIDN:AAA35825.1; PID:g292023  
A;Note: splice form B1  
A;Accession: I70303  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-10,103-153,'A',155-280 <RE2>  
A;Cross-references: GB:I03420; NID:g182461; PIDN:AAA35826.1; PID:g292024  
A;Experimental source: mononuclear cells  
A;Note: splice form B2  
C;Comment: This receptor does not bind monomeric IGG with high affinity.  
C;Genetics:  
A;Gene: GDB:FCGR1B; CD64  
A;Cross-references: GDB:135923; OMIM:601502  
A;Map position: lp12-1p12  
C;Superfamily: Fc gamma receptor I; immunoglobulin homology  
C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane F;  
F;117-170/Domain: immunoglobulin homology <IMW>

Query Match 35.0%; Score 375.5; DB 2; Length 280;  
Best Local Similarity 41.7%; Pred. No. 8.4e-23;  
Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVTLTCGNNFFVSVSTKWFHNGSL 70  
DB 4 LITLLLVWVVDGQVDT-KKAVITLQPPWVSFQEEVTILHCEVLHLPQSSSTQWFLNGTA 62

QY 71 SEETNSLNIIVNAKFDSEGEYKCOHQOVNESPVLYLEFSDWLLLOQASAEVVMGQPLFL 130  
DB 63 TOTSTPSYRITASVNDSEYRCQGLSGRSDPIQLEIHRGWLMLLOQVSRVFMGEPLAL 122



A:Reference number: S46999; MUID:94349933; PMID:8070412

A:Accession: S46999

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <PEI>

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor; transmembrane protein

F:130-183/Domain: immunoglobulin homology <IMM2>

Query Match 34.1%; Score 366; DB 2; Length 261;

Best Local Similarity 40.5%; Pred. No. 4.4e-22;

Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGVAVPQPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNG-S 69

DB 16 LTLLFFAFADPQSAALPKAVVLDPPWQVLKEDMTLMCEGTHNPGNSSTQWFHNGS 75

QY 70 LSEETNSLINVAKFEDSGEYKQHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLF 129

DB 76 IRSQWASVTF-KATVNDSGEYRCQMEQTRUSDVGLVSDWLLLOTQPVFLEGETIT 134

QY 130 LRCHGWRNDVYKVIYKDGALKYWYENHISITNAIVEDSGTYCTGKVMQLDYSESP 189

DB 135 LRCHSWRNKLNIRISFFHNKSVRYHYKSNFSIPKANHSFGDYCKGSLGSTQHQSKP 194

QY 190 LNIIV 194

DB 195 VTIV 199

#### RESULT 13

Fc gamma (IgG) receptor type 2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

A:Accession: S36903

R:Bocek, P.; Pecht, I.

FEBS Lett. 331. 86-90. 1993

A:Title: Cloning and sequence of the cDNA coding for rat type II Fc-gamma receptor of ma

A:Reference number: S36903; MUID:94009652; PMID:8405417

A:Accession: S36903

A:Molecule type: mRNA

A:Residues: 1-285 <BOC>

A:Cross-references: EMBL:X73371; NID:G397576; PIDN:CAA51788.1; PID:G397577

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: immunoglobulin receptor

F:52-103/Domain: immunoglobulin homology <IMV>

Query Match 34.0%; Score 364.5; DB 2; Length 285;

Best Local Similarity 38.9%; Pred. No. 6.5e-22;

Matches 72; Conservative 36; Mismatches 76; Indels 1; Gaps 1;

QY 10 LLCVALFFAPDGVAVPQPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGS 69

DB 19 LLTAVNLVAESAGLP-KAVVXLEPPWQVLKEDTVMCEGTHNPKNCSTQWFHNGS 77

QY 70 LSEETNSLINVAKFEDSGEYKQHQVNESEPVYLEVFSDFWLLQASAEVVMGQPLF 129

DB 78 SIWHAQANYTFKATVNDSGEYRCMEETGISEPIHLGLVSDWLLLOTQVLEGETIT 137

QY 130 LRCHGWRNDVYKVIYKDGALKYWYENHISITNAIVEDSGTYCTGKVMQLDYSESP 189

DB 138 LRCHSWRNKLNIRISFFHNKSVRYHYKSNFSIPKANHSFGDYCKGSLGSTQHQSKP 197

QY 190 LNIIV 194

DB 195 VTIV 202

#### RESULT 14

JU0284

Fc gamma (IgG) receptor III-B precursor (neutrophil) - human

N:Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra

C:Species: Homo sapiens (man)

C:Date: 07-Sep-1990 #sequence\_revision 02-Aug-1996 #text\_change 28-Jan-2000

A:Accession: JU0284; S00758; I37628; B32933; A31460

R:Ravetch, J.V.; Perussia, B.

J. Exp. Med. 170. 481-497. 1989

A:Title: Alternative membrane forms of Fc gamma RIII (CD16) on human natural killer cells

A:Reference number: JLO107; MUID:89328325; PMID:2526946

A:Accession: JU0284

A:Molecule type: mRNA

A:Residues: 1-201, 'SP', 204-233 <RAV>

A:Cross-references: GB:J04162

A:Note: the sequence of the receptor from human NK cells, reported in the same paper, di

rboxyl end

R:Simmons, D.; Seed, B.

Nature 333. 568-570. 1988

A:Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane

A:Reference number: S00758; MUID:88232937; PMID:2967436

A:Accession: S00758

A:Molecule type: mRNA

A:Residues: 1-233 <SIM>

A:Cross-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745

R:Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.

J. Biol. Chem. 270. 1350-1361. 1995

A:Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole

A:Reference number: A55439; MUID:95138331; PMID:7836402

A:Accession: I37628

A:Molecule type: DNA

A:Residues: 1-72 <RES>

A:Cross-references: EMBL:246223; NID:G559446; PIDN:CAA86296.1; PID:G871306

R:Scallon, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.

Proc. Natl. Acad. Sci. U.S.A. 86. 5079-5083. 1989

A:Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph

A:Reference number: A32933; MUID:89296947; PMID:2525780

A:Accession: B32933

A:Molecule type: mRNA

A:Residues: 1-121, 'E', 123-150, 'S', 152-233 <SCA>

A:Cross-references: GB:M24854; NID:G184851; PIDN:AAA53507.1; PID:G306930

R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.

Proc. Natl. Acad. Sci. U.S.A. 86. 1013-1017. 1989

A:Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal

A:Reference number: A31460; MUID:89128938; PMID:2521732

A:Accession: A31460

A:Molecule type: mRNA

A:Residues: 1-35, 'R', 37-64, 'N', 66-81, 'D', 83-105, 'V', 107-233 <PEL>

A:Cross-references: GB:J04162; NID:G183036; PIDN:AAA35881.1; PID:G183037

C:Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the

I, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod

C:Genetics:

A:Gene: GDB:FCGR3B; FCG3; FCGR3

A:Cross-references: GDB:128176; OMIM:146740

A:Map position: 1Q23-1Q23

A:Introns: 14/1, 21/1

A:Note: the list of introns is incomplete

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <IAT>

F:40-91/Domain: immunoglobulin homology <IMM1>

F:111-174/Domain: immunoglobulin homology <IMM2>

F:56.63,82,92,180.187/Binding site: carbohydrate (asn) (covalent) #status predicted

F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 33.9%; Score 363.5; DB 1; Length 233;

Best Local Similarity 42.8%; Pred. No. 6.2e-22;

Matches 80; Conservative 26; Mismatches 78; Indels 3; Gaps 2;

QY 10 LLCVALFFAPDGVAVPQPKK--VSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHFN 67

DB 5 LLPTALLLVASG-MRTEDLPKAVVLEPQWYSVLEKDSVTLKCCGAYSPEDNSTQWFHN 63

QY 68 GSLSEETNSLINVAKFEDSGEYKQHQVNESEPVYLEVFSDFWLLQASAEVVMGQOP 127

DB 64 ESLISSQASSYFIDAAATVNDSGEYRCQTNLTSLSDPVLQLEVHICWLLQLQAPRWFKEDP 123



QY	128	LFLRCHGWRNWDVVKVIYYKDGGEALKWYNHNHISITNATVDSGTTCYCTGGKWOLDYES	187
DB	124	THLRCHSWKNTALHKVTYLQNGDKORYFHNSDFHIPKATLKDSGSIFCRGLVGSKNVSS	183
QY	188	EPLNITY	194
DB	184	ETVNITI	190

## RESULT 15

I56110  
Fc-gamma RIIB-alpha - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jan-2000  
C:Accession: I56110  
R:Farber, D.L.; Sears, D.W.  
J. Immunol. 146, 4352-4361, 1991  
A:Title: Rat Cdl6 is defined by a family of class III Fc-gamma receptors requiring co-ex  
A:Reference number: I56110; MUID:91250730; PMID:1710249  
A:Accession: I56110  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-267 <RES>  
A:Cross-references: GB:M64369; NID:g206674; PIDN:AAA42048.1; PID:g2066675  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
F:55-106/Domain: immunoglobulin homology <IMM>

Query Match 33.7%; Score 362; DB 2; Length 267;  
Best Local Similarity 39.7%; Pred. No. 9.5e-22;  
Matches 73; Conservative 34; Mismatches 77; Indels 0; Gaps 0;

Qy	11	LCVALLFPAPDGLVAPQPKVSLNPWRIFKENVTILTCNGNNFFVSVSTKWFHNSGL	70
Db	22	LTMLLLFAFADRTANLPAKVYKRDPPMIQVLKEDTTLTCEGTHNPGNSSTOWPHNQSS	81
Qy	71	SEETNSSLNINAKPEDESGEYKCOHQQVNESEPVYLEVFSDWLLLLQASAEVVMGQPLFL	130
Db	82	TGQVQVQASYTFKATVNDSGEYRCMAHTSLSDPILHLEVISDWLLLLQTPQLVPEEGTITL	141
Qy	131	RCHGRNRNDVYKVIYKDKGEALKYWEYENHNISITNATVEDSGTYTCYTKGWQLDYSEPL	190
Db	142	RCHSMWKQLTKVLLFQNGKPVRYYYQSSNFSIPKANHSHSGNYCYCKAYLGRTHMVSKDV	201
Qy	191	NTTV	194
Db	202	TITV	205

Search completed: October 6, 2004, 09:23:43  
Job time : 11.7914 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 6.65851 Seconds  
(without alignments)  
1540.558 Million cell updates/sec

Title: US-10-763-400-11

Perfect score: 1073  
Sequence: 1 MAPANESPTLLCVALLFPAP.....GKWLQDYSEPLNITVIKA 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	257	1 FCEA_HUMAN	P12319 homo sapien
2	511	47.6	250	1 FCEA_MOUSE	P20489 mus musculus
3	489	45.6	245	1 FCE1_RAT	P12371 rattus norv
4	405	37.7	296	1 FCG2_BOVIN	Q28110 bos taurus
5	387.5	36.1	341	1 FCG2_CAVPO	Q60513 cavia porce
6	379	35.3	374	1 FCG1_HUMAN	P12314 homo sapien
7	379	35.3	404	1 FCG1_MOUSE	P26151 mus musculus
8	368.5	34.3	250	1 FCG3_BOVIN	P79107 bos taurus
9	368	34.3	257	1 FCG3_PIG	Q28942 sus scrofa
10	367.5	34.2	254	1 FCG3A_HUMAN	P08637 homo sapien
11	365	34.1	261	1 FCG3_MOUSE	P08508 mus musculus
12	364.5	34.0	285	1 FCG2_RAT	Q63203 rattus norv
13	363.5	33.9	233	1 FCG3_HUMAN	O75015 homo sapien
14	363	33.8	267	1 FCG3_RAT	P27645 rattus norv
15	361.5	33.7	310	1 FCG3B_HUMAN	P31994 homo sapien
16	361.5	33.7	323	1 FCGC_HUMAN	P31995 homo sapien
17	357.5	33.3	330	1 FCG2_MOUSE	P08101 mus musculus
18	348.5	32.5	316	1 FCGA_PANTR	O8spv8 pan troglod
19	348	32.4	157	1 FCE2_RAT	P12840 rattus norv
20	347	32.3	317	1 FCGA_HUMAN	P12318 homo sapien
21	172	16.0	1709	1 SN_HUMAN	Q9B222 homo sapien
22	164.5	15.3	1694	1 SN_MOUSE	P62230 mus musculus
23	152	14.2	422	1 K3L1_RAT	P83556 rattus norv
24	144	13.4	432	1 K3L1_MOUSE	P83555 mus musculus
25	136.5	12.7	521	1 CEAL_MOUSE	P31809 mus musculus
26	135	12.6	837	1 NCM2_MOUSE	O35136 mus musculus
27	130	12.1	519	1 ECTO_RAT	P16573 rattus norv
28	128.5	12.0	344	1 CEAG_HUMAN	P40199 homo sapien
29	126.5	11.8	1302	1 NRG_DROME	P20241 drosophila
30	125.5	11.7	978	1 KFM5_RAT	Q00495 rattus norv
31	124.5	11.6	977	1 KFM5_MOUSE	P09581 mus musculus
32	120	11.2	702	1 CEAS_HUMAN	P06731 homo sapien
33	120	11.2	6632	1 UN89_CAEEL	O01751 caenorhabdi

34 118 11.0 458 1 CD4\_MACNE  
35 117.5 11.0 837 1 NCM2\_HUMAN  
36 117.5 11.0 847 1 CD22\_HUMAN  
37 117 10.9 1197 1 CAM1\_BRARE  
38 116 10.8 458 1 CD4\_CERAB  
39 116 10.8 1240 1 NFAS\_HUMAN  
40 116 10.8 3707 1 FGBM\_MOUSE  
41 114.5 10.7 344 1 NTRI\_HUMAN  
42 114.5 10.7 344 1 NTRI\_MOUSE  
43 114.5 10.7 344 1 NTRI\_RAT  
44 113.5 10.6 1021 1 CONT\_RAT  
45 113 10.5 458 1 CD4\_MACFA

#### ALIGNMENTS

RESULT 1  
FCEA\_HUMAN  
ID\_FCEA\_HUMAN STANDARD; PRT; 257 AA.  
AC P12319;  
DI 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, last sequence update)  
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor  
DE (FCERI) (Ige Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).  
GN FCER1A OR FCE1A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88233953; PubMed=2967464;  
RA Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;  
RT "Isolation of the gene coding for the alpha subunit of the human high  
RT affinity Ige receptor.";  
RL Nucleic Acids Res. 16:3584-3584(1988).  
RN [2]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Maat cells;  
RX MEDLINE=88158102; PubMed=2964640;  
RA Shimizu A., Repler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,  
R Leder P.;  
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:  
RT characterization of putative alpha-chain gene products.";  
Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).  
RN [3]  
RP 3D-STRUCTURE MODELING OF 26-197.  
RX MEDLINE=93113350; PubMed=1472946;  
RA Padlan E.A., Helm B.A.;  
RT "A modeling study of the alpha-subunit of human high-affinity  
RT receptor for immunoglobulin-E.";  
Receptor 2:129-144(1992).  
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH  
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC  
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL  
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)  
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR  
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.  
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO  
CC DISULFIDE LINKED GAMMA CHAINS.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; X06948; CAA30025.1; -  
 DR EMBL; J03605; AAA36204.1; -  
 DR EMBL; A21606; CRA01564.1; -  
 DR PIR; S00682; S00682.  
 DR PDB; 1ALS; 27-FEB-95.  
 DR PDB; 1ALT; 27-FEB-95.  
 DR PDB; 1F2Q; 08-JUN-00.  
 DR PDB; 1J86; 29-AUG-01.  
 DR PDB; 1J87; 29-AUG-01.  
 DR PDB; 1J88; 29-AUG-01.  
 DR PDB; 1J89; 05-SEP-01.  
 DR Genew; HGNC:3609; FCER1A.  
 DR MIM; 147140; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00408; IgC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR IGB-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; 3D-structure.  
 FT SIGNAL 1 25  
 FT CHAIN 26 257  
 FT HIGH AFFINITY IMMUNOGLOBULIN EPSILON  
 FT RECEPTOR ALPHA-SUBUNIT  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE 1.  
 FT DOMAIN 30 110  
 FT DOMAIN 111 193  
 FT DISULFID 51 93  
 FT DISULFID 132 176  
 FT CARBOHYD 46 46  
 FT CARBOHYD 67 67  
 FT CARBOHYD 75 75  
 FT CARBOHYD 99 99  
 FT CARBOHYD 160 160  
 FT CARBOHYD 165 165  
 FT CARBOHYD 191 191  
 FT STRAND 31 35  
 FT HELIX 39 42  
 FT TURN 43 43  
 FT STRAND 48 54  
 FT STRAND 61 66  
 FT TURN 67 68  
 FT STRAND 69 71  
 FT STRAND 74 74  
 FT TURN 75 76  
 FT STRAND 77 79  
 FT HELIX 82 87  
 FT STRAND 91 96  
 FT TURN 98 100  
 FT TURN 101 101  
 FT STRAND 104 107  
 FT STRAND 114 116  
 FT HELIX 120 124  
 FT STRAND 128 133  
 FT STRAND 143 145  
 FT STRAND 146 148  
 FT TURN 149 149  
 FT STRAND 150 150  
 FT TURN 152 153  
 FT STRAND 154 155  
 FT TURN 156 159  
 FT STRAND 160 163  
 FT HELIX 165 170  
 FT STRAND 175 178  
 FT STRAND 181 182  
 FT TURN 183 185  
 FT STRAND 186 187  
 FT STRAND 190 193  
 SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;

Query Match

100.0%; Score 1073; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.5e-86;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRPKGNVTLTNGNNFFFEVS 60  
 DB 1 MAPAMESPTLLCVALLFPAPDGLAVPQPKVSLNPPNRPKGNVTLTNGNNFFFEVS 60  
 QY 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQCVNESEPVYLEVFSWMLLQASAE 120  
 DB 61 STKWFHNGSLSEETNSSLNINAKFEDSGEYKCHQCVNESEPVYLEVFSWMLLQASAE 120  
 QY 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGALKYWYENHNSITNATVEDSGTYCTGKV 180  
 DB 121 VMEGQPLFLRCHGWRNWDVYKVIYKDGALKYWYENHNSITNATVEDSGTYCTGKV 180  
 QY 181 WOLDYSEPLNITVIKA 197  
 DB 181 WOLDYSEPLNITVIKA 197  
 RESULT 2  
 FCEA MOUSE STANDARD; PRT; 250 AA.  
 ID\_FCEA\_MOUSE  
 AC P20489;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor  
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).  
 GN FCER1A OR FCE1A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89359361; PubMed=2527850;  
 RA Ra C., Jouvin M.H.E., Kinet J.-P.;  
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc  
 epsilon RI) and surface expression of chimeric receptors  
 RT (rat-mouse-human) on transfected cells.";  
 RL J. Biol. Chem. 264:15323-15327(1989).  
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH  
 CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC  
 CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL  
 CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)  
 CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR  
 CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.  
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO  
 CC DISULFIDE LINKED GAMMA CHAINS.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.  
 CC  
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 CC  
 CC EMBL; J05018; AAA37600.1; -  
 DR PIR; A34342; A34342.  
 DR HSSP; P12319; 1ALS.  
 DR MGD; MGI:95494; Pcer1a.  
 DR GO; GO:0007165; P:signal transduction; IDA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003599; IG.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR IGB-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat.

FT SIGNAL 1 23  
FT CHAIN 24 250  
FT DOMAIN 24 204  
FT TRANSMEM 205 223  
FT DOMAIN 224 250  
FT DOMAIN 28 104  
FT DOMAIN 114 181  
FT DISULFID 49 92  
FT DISULFID 131 174  
FT CARBOHYD 58 58  
FT CARBOHYD 66 66  
FT CARBOHYD 73 73  
FT CARBOHYD 106 106  
FT CARBOHYD 152 152  
FT CARBOHYD 167 167  
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BF84DC0C4E CRC64;

Query Match 47.6%; Score 511; DB 1; Length 250;  
Best Local Similarity 51.1%; Pred. No. 1.5e-37;  
Matches 96; Conservative 38; Mismatches 52; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGVAVPQKPVSLNPPWIRIFKGVNTLCNGNNFV-SSTKWFHNGS 69  
DB 9 LCLALLFMSLDVILFATEKSVLTLDPPWIRIFTEGKVTLCYGNHLOQNMSTTKWIHNGT 68  
QY 70 LSEETNSLINVNAKFEDSGYKCOHQVNESEPVLEFSDMLLQASAEVVMGQPLF 129  
DB 69 VSEVNSHLVIVSATVDSQKGYCQKQLFKSKPVLYNVTCQDMLLQTSADMLVHGSFD 128  
QY 130 LECHGRWVDYKVIYKDGKALFYWHNHNISITNATVEDSGTYCTGKVMQLDYSEPL 189  
DB 129 IRCHGKWNVRKVIYRDNHAFNYSVES-PVSREATLNDSGTYHCKYLRQVEYSDK 187  
QY 190 LNIITVKA 197  
DB 188 FRIAVVKA 195

RESULT 3  
ID FCEL RAT STANDARD; PRT; 245 AA.  
AC P12371;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor  
DE (FCRI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).  
GN FCRI OR FCRI.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86024987; PubMed=2959318;  
RA Kinet J.-P., Metzger H., Hakimi J., Kochan J.;  
RT "A cDNA presumptively coding for the alpha subunit of the receptor  
RT with high affinity for immunoglobulin E";  
RL Biochemistry 26:4605-4610(1987).  
RN [2]  
RP REVISIONS.  
RA Kochan J.;  
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Test cells;  
RX MEDLINE=88158102; PubMed=2964540;  
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,  
RA Leder P.;  
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:  
RT characterization of putative alpha-chain gene products.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).

RN [4]  
RP SEQUENCE OF 21-245 FROM N.A.  
RX MEDLINE=88289772; PubMed=2969594;  
RA Liu F.-T., Albrandt K., Robertson M.W.;  
RT "cDNA heterogeneity suggests structural variants related to the high-  
RT affinity IgE receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).  
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH  
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC  
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL  
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)  
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR  
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.  
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO  
CC DISULFIDE LINKED GAMMA CHAINS.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.  
CC  
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CC  
CC EMBL; M17153; AAA42045.1; -;  
CC EMBL; J03606; AAA41582.1; -;  
CC EMBL; M21822; AAA41146.1; -;  
CC FIR; C31327; A30154.  
CC HSP; P12319; IALS.  
CC InterPro; IPR007110; Ig-like.  
CC InterPro; IPR003599; Ig.  
CC Pfam; PF00047; Ig; 2.  
CC SMART; SM00409; Ig; 2.  
CC PROSITE; PS50835; IG LIKE; 1.  
CC IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Immunoglobulin domain; Repeat.  
FT SIGNAL 1 23  
FT CHAIN 24 245  
FT DOMAIN 24 204  
FT TRANSMEM 205 223  
FT DOMAIN 224 245  
FT DOMAIN 28 103  
FT DOMAIN 113 181  
FT DISULFID 49 91  
FT DISULFID 130 174  
FT CARBOHYD 52 52  
FT CARBOHYD 53 53  
FT CARBOHYD 58 58  
FT CARBOHYD 65 65  
FT CARBOHYD 123 123  
FT CARBOHYD 158 158  
FT CARBOHYD 167 167  
SQ SEQUENCE 245 AA; 27793 MW; A0E67DD363B72197 CRC64;

Query Match 45.6%; Score 489; DB 1; Length 245;  
Best Local Similarity 48.9%; Pred. No. 1.2e-35;  
Matches 91; Conservative 37; Mismatches 58; Indels 0; Gaps 0;

QY 11 LCVALFFAPDGVAVPQKPVSLNPPWIRIFKGVNTLCNGNNFV-SSTKWFHNGSL 70  
DB 9 LCLALLFMSLDVILFATEKSVLTLDPPWIRIFTEGKVTLCYGNHLOQNMSTTKWIHNDGI 68  
QY 71 SEETNSLINVNAKFEDSGYKCOHQVNESEPVLEFSDMLLQASAEVVMGQPLF 130  
DB 69 SNVSKSHVIVSATIQSGKIICQKGFYKSKPVLYNVVMQEMLLQSSADVLDNGSGFDI 128  
QY 131 RCHGRWVDYKVIYKDGKALFYWHNHNISITNATVEDSGTYCTGKVMQLDYSEPL 190  
DB 129 RCRSWKWKVKVIYKDDIAFKYSYDNNISIRKATFNDSGSYHCTGYLNKVECKSKF 188

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QY 191 NITVIX 196
Db 189 SIATVK 194

RESULT 4
FCG2_BOVIN STANDARD; PRT; 296 AA.
AC Q28110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
gamma RII) (FCRII) (IgG Fc receptor II).
GN FCGR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=94245284; PubMed=8189320;
RA Zhang G., Young J.R., Tregaskes C.R., Howard C.J.;
RA "Cattle Fc gamma RII: molecular cloning and ligand specificity.";
RL Immunogenetics 39:423-427(1994).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Higher expression is found in macrophages than
CC in neutrophils (Probable).
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; X75671; CAA53367.1; -.
CC PIR; I46021; I45021.
CC HSSP; P12319; 1ALS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; Ig; 2.
CC PROSITE; PS0835; Ig_LIKE; 2.
CC Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat.
CC SIGNAL 1 42
CC CHAIN 43 296
CC LOW AFFINITY IMMUNOGLOBULIN GAMMA Fc
CC REGION RECEPTOR II.
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM
CC DOMAIN 226 246
CC DOMAIN 247 296
CC DOMAIN 47 129
CC DOMAIN 130 212
CC SITE 273 278
CC SITE 70 112
CC DISULFID 151 195
CC DISULFID 79 79
CC CARBOHYD 86 86
CC CARBOHYD 105 105
CC CARBOHYD 179 179
CC CARBOHYD 186 186
CC CARBOHYD 210 210

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SQ SEQUENCE 296 AA; 33020 MW; A61A40A611F71ED5 CRC64;
Query Match 37.7%; Score 405; DB 1; Length 296;
Best Local Similarity 42.2%; Pred. No. 3.3e-28;
Matches 79; Conservative 33; Mismatches 71; Indels 4; Gaps 2;

QY 10 LLCVALLFPAPDGVLAVPQPK--VSLNPPWNRIFKGENVILTCNGNPFVSSVTKWFHN 67
Db 29 LLWTALLFLAP--VSGKPLPKAVVTIQPAWINVLREDEHVTLCQGTSTFSAGNLTWFHN 86
QY 68 GSLSEETSSNLIVNAKPEDSGEYKQHQOVNESPVLYEFSDMLLQASAEVVMGEP 127
Db 87 GSSIIHQPKPSYFRAGSNDSSYRCOREQTSLSDFVHLVDVSDMLLQTSLSLVEQSEEP 146
QY 128 LFIKCHGRNWDVYKVIYKDGKALKYWENHINISITATVEDSGTYCTGKMWOLDYES 187
Db 147 IMLRCHSWENQPLNKITFYQDRKSKIFSYQRTNFSIPRANLSHQYHCTAFIGKMLHSS 206
QY 188 EPLNITV 194
Db 207 QPWNITV 213

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RESULT 5
FCG2_CAVPO STANDARD; PRT; 341 AA.
AC Q60513; Q60498; Q60511; Q60512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
gamma RII) (FCRII) (IgG Fc receptor II) (Fc-gamma-1/gamma-2 receptor).
GN FCGR2.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=90241239; PubMed=1692213;
RA Tominaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
RA "The structure and expression of the guinea pig Fc receptor for IgG1
RT and IgG2 (Fc gamma 1/gamma 2R).";
RL Biochem. Biophys. Res. Commun. 168:683-689(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
RC STRAIN=JY-1;
RC MEDLINE=93346746; PubMed=8345193;
RA Yamashita T., Shinozaki K., Yamashita Y.;
RA "Expression cloning of complementary DNA encoding three distinct
RT isoforms of guinea pig Fc receptor for IgG1 and IgG2.";
RL J. Immunol. 151:2014-2023(1993).
CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=2R-B3;
CC IsoId=Q60513-1; Sequence=Displayed;
CC Name=2R-B1;
CC IsoId=Q60513-2; Sequence=VSP_002639;
CC Name=2R-B2;
CC IsoId=Q60513-3; Sequence=VSP_002638;
CC -!- TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes
CC express preferentially isoform 2R-B1. B lymphocytes express
CC isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC -----
CC EMBL; X75671; CAA53367.1; -.
CC PIR; I46021; I45021.
CC HSSP; P12319; 1ALS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; Ig; 2.
CC PROSITE; PS0835; Ig_LIKE; 2.
CC Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
CC Immunoglobulin domain; Repeat.
CC SIGNAL 1 42
CC CHAIN 43 296
CC LOW AFFINITY IMMUNOGLOBULIN GAMMA Fc
CC REGION RECEPTOR II.
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM
CC DOMAIN 226 246
CC DOMAIN 247 296
CC DOMAIN 47 129
CC DOMAIN 130 212
CC SITE 273 278
CC SITE 70 112
CC DISULFID 151 195
CC DISULFID 79 79
CC CARBOHYD 86 86
CC CARBOHYD 105 105
CC CARBOHYD 179 179
CC CARBOHYD 186 186
CC CARBOHYD 210 210

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
[1]  
SEQUENCE FROM N.A. [NCBI TaxID=9606](#)

Allen J.M., Seed B.;  
"Nucleotide sequence of three cDNAs for the human high affinity Fc  
receptor (FcRI)".  
Nucleic Acids Res. 16:11824-11824(1988).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=89100284, PubMed=2911749;  
Allen J.M., Seed B.;  
"Isolation and expression of functional high-affinity Fc receptor  
complementary DNAs".  
Science 243:378-381(1989).

```

--!- FUNCTION: Binds to the FC region of immunoglobulin gamma. High
      affinity receptor.
--!- SUBCELLULAR LOCATION: Type I membrane protein.
--!- ALTERNATIVE PRODUCTS:
      Event=Alternative splicing; Named isoforms=2;
      Name=A;
      IsoId=PI2314-1; Sequence=Displayed;

```

```

Name=B;
ISOID=P12314-2; Sequence=VSP_002637;
-- ITSSUE SPECIFICITY: Monocyte/macrophage specific.
-- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-- DATABASES: NAME=PROW; NAME=CD64 entry;
WWW='http://www.ncbi.nlm.nih.gov/prow/cd/cd64.htm'.

```

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EMBL; X14356; CAA32537.1; --  
EMBL; X14355; CAA32536.1; --  
PIR; A41357; A41357.  
HSSP; P12319; IALS.  
Genew; HGNC:3613; FCGR1A.

MIM; 148760; -. P:receptor signaling protein activity; TAS.  
 GO: GO:0005057; P:receptor signaling protein activity; TAS.  
 GO: GO:0006955; P:immune response; TAS.  
 GO: GO:0006911; P:phagocytosis, engulfment; TAS.  
 GO: GO:0007165; P:signal transduction; TAS.  
 InterPro: IPR007110; IG-like.  
 InterPro: IPR003599; IG.  
 Pfam: PF00047; IG; 3.  
 SMART: SMC0409; IG; 3.  
 PROSITE: PS50835; IG LIKE; 3.  
 IGF-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 Transmembrane domain; Receptor; Alternative splicing; Polymorphism.

SIGNAL CHAIN	22	374
IMMUNOGLOBULIN DOMAIN	1	21
HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I.	22	392
POTENTIAL.	22	292
EXTRACELLULAR (POTENTIAL).	293	313
POTENTIAL.	293	313
CYTOPLASMIC (POTENTIAL).	314	374
IG-LIKE C2-TYPE 1.	22	101
IG-LIKE C2-TYPE 2.	95	184

DOMAIN	190	277	IG-LIKE C2-TYPE 3.
DISULFID	43	85	BY SIMILARITY.
DISULFID	124	168	BY SIMILARITY.
DISULFID	212	260	BY SIMILARITY.
CARBOHYD	59	59	N-LINKED (GLCNAC. .)
CARBOHYD	78	78	N-LINKED (GLCNAC. .)
CARBOHYD	152	152	N-LINKED (GLCNAC. .)
CARBOHYD	159	159	N-LINKED (GLCNAC. .)
CARBOHYD	163	163	N-LINKED (GLCNAC. .)









Query Match 34.2%; Score 367.5; DB 1; Length 254;  
Best Local Similarity 42.8%; Pred. No. 5.1e-25;  
Matches 80; Conservative 27; Mismatches 77; Indels 3; Gaps 2;

10 LLVALLFPADGVLAVPQPK--VSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG 67  
5 LLPTALLLLVSAG-MRTEDLPKAVVFLPEQWRYLLEKSDVTLKCCQAYSFEDNSTQWFH 63  
68 GSLSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 127  
64 ESLLSQASSYFIDAAVTDDSGEYRCQTNLSTLSDPVQLEVHIGWLLQLQAPRWVKEEDP 123  
128 LFLCHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
124 IHLRCHSWKNTALHKVTVLQNGKGRKYFHNSDPYIPKATLKDSGYSFCRGLFGSKNVSS 183

188 EPLNITV 194  
184 ETVNITV 190

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQWFHNGRS 75  
70 LSEETNSLNIIVNAKFDSDGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPL 129  
76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVLGVIDSWLLQLQTPQVFLGETIT 134  
130 LECHGRWNVKVIYKIDGALKWYENHNISITNATVEDSGYVCTGKWLQDYSE 189  
135 LRCHSWRNLNLRISFFHNEKSVRIHYKSNFSPKANHSIGSDYCKGSLGSGTQHQSKP 194

190 LMITV 194  
195 VMITV 199

Query Match 34.1%; Score 366; DB 1; Length 261;  
Best Local Similarity 40.5%; Pred. No. 7.2e-25;  
Matches 75; Conservative 32; Mismatches 76; Indels 2; Gaps 2;

11 LCVALLFPADGVLAVPQPKVSLNPPWNRIFKGVNTLTCNGNPFVSVSTKWFHNG-S 69  
16 JTILLFADFADQSAALPKAVVKLDPPWIVLKEDMTLCEGTHNPGNSSTQ

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; X73371; CAA51788.1; -;  
DR PIR; S36903; S36903.  
DR HSP; F12319; IALS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003599; Ig.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 2.  
DR PROSITE; PS50835; IG LIKE; 2.  
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Immunoglobulin domain; Repeat.  
FT SIGNAL 1 31  
FT CHAIN 32 285

FT DOMAIN 32 212  
FT TRANSMEM 213 233  
FT DOMAIN 234 285  
FT DOMAIN 36 118  
FT DOMAIN 119 201  
FT SITE 262 267  
FT DISULFID 59 101  
FT DISULFID 140 184  
FT CARBOHYD 67 67  
FT CARBOHYD 75 75  
FT CARBOHYD 86 86  
FT CARBOHYD 94 94  
FT CARBOHYD 168 168  
FT CARBOHYD 175 175  
SQ SEQUENCE 285 AA; 3204 MW; 255540A584CFFA0A CRC64;

Query Match 34.0%; Score 364.5; DB 1; Length 285;  
Best Local Similarity 38.9%; Pred. No. 1.1e-24;  
Matches 72; Conservative 36; Mismatches 76; Indels 1; Gaps 1;  
QY 10 LLVALLFFAPDGLVLPQPKVSLNPPNRIKGVNVTLCNKNPFVSSSTKWFHNGS 69  
DB 19 LLTAVNLVAESHAGLP-KAVVLEPPWQVLKEDVTLMCEGTHTKNCSTQWFHNGS 77  
QY 70 LSEETNSLNLVNAKFDSEGEYKQHQOVNESEPVYLEVFSDDLLOQASAEVNVNQPLF 129  
DB 78 SIMHQQAQNYTFKATVNDSDGEYRCMEETGISEPIHLGVISDWLLQTSQLVPEGETIT 137  
QY 130 LRCHGRNDVYKVIYKDGKALYVYENHNISITNATVDSGTGYCTGKVQWLDYESEP 189  
DB 138 LRCHSWKQQLTKVLLFQNGKPVRYHQSNFSPKXNHSNGYNYCKAYLGRMTVSKP 197  
QY 190 LNIIV 194  
DB 198 VTIV 202

RESULT 13  
ID FC3B HUMAN STANDARD; PRT; 233 AA.  
AC 075015;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Low affinity immunoglobulin gamma Fc region receptor III-B precursor  
DE (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIB)  
DE (FCRIIB) (Fc-gamma RIII) (FCRII) (CD16-B) (FCR-10).  
GN FCR3B OR FCG3 OR FCG3R OR IGR3 OR CD16B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (VARIANT NA-2).  
RX MEDLINE=89328325; PubMed=2526846;

RA Ravetch J.V., Perussia B.;  
RT "Alternative membrane forms of Fc gamma RIII(CD16) on human natural  
RT killer cells and neutrophils. Cell type-specific expression of two  
RT genes that differ in single nucleotide substitutions.";  
RL J. Exp. Med. 170:481-497(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (VARIANT NA-2).  
RC TISSUE=Placenta;  
RX MEDLINE=88232937; PubMed=2967436;  
RA Simmons D., Seed B.;  
RT "The Fc gamma receptor of natural killer cells is a phospholipid-  
RT linked membrane protein";  
RL Nature 333:568-570(1988).  
RN [3]  
RP ERRATUM.  
RA Simmons D., Seed B.;  
RL Nature 340:662-662(1989).  
RN [4]  
RP SEQUENCE FROM N.A. (VARIANT NA-1).  
RC TISSUE=Leukocyte;  
RX MEDLINE=89128838; PubMed=2521732;  
RA Peltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;  
RT "Human Fc-gamma-RIII: Cloning, expression, and identification of the  
RT chromosomal locus of two Fc receptors for IgG.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).  
RN [5]  
RP SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).  
RC TISSUE=Placenta;  
RX MEDLINE=95138131; PubMed=7836402;  
RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;  
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B  
RT genes. Molecular characterization of the promoter regions.";  
RL J. Biol. Chem. 270:1350-1361(1995).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 FC.  
RX MEDLINE=20372189; PubMed=10917521;  
RA Sondermann P., Huber R., Oosthuizen V., Jacob U.;  
RT "The 3.2-A crystal structure of the human IgG1 Fc fragment-Fc  
RT gammaRIII complex.";  
RL Nature 406:267-273(2000).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.  
RX MEDLINE=20471519; PubMed=11021536;  
RA Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,  
RA Santes-Fridman C., Sun P.D.;  
RT "Crystal structure of the extracellular domain of a human Fc gamma  
RT RIII.";  
RL Immunity 13:387-395(2000).  
RN [8]  
RP VARIANT SH ASP-78.  
RX MEDLINE=97180159; PubMed=9028335;  
RA Bux J., Stein E.L., Bierling P., Fromont P., Clay M., Stroncek D.,  
RA Santoso S.;  
RT "Characterization of a new alloantigen (SH) on the human neutrophil Fc  
RT gamma receptor IIIB.";  
RL Blood 89:1027-1034(1997).  
CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW  
CC AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO  
CC MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE  
CC ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A  
CC TRAP FOR IMMUNE COMPLEXES IN THE PERIPHERAL CIRCULATION WHICH DOES  
CC NOT ACTIVATE NEUTROPHILS.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC EXISTS ALSO AS A SOLUBLE RECEPTOR, PRODUCED BY A PROTEOLYTIC  
CC CLEAVAGE.  
CC -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY BY POLYMORPHONUCLEAR  
CC LEUKOCYTES (NEUTROPHILS). ALSO EXPRESSED BY STIMULATED  
CC EOSINOPHILS.  
CC -!- PTM: GLYCOSYLATED. GLYCOSYLATION PLAYS AN INHIBITORY ROLE IN THE  
CC INTERACTION WITH IGG3.  
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.  
CC -!- POLYMORPHISM: There are three allelic forms of FCR3B: NA-1, NA-2

CC (shown here) and SH. NA-1 and NA-2 are detectable with antibodies  
 CC against the biallelic neutrophil-specific antigen system NA.  
 CC -!- DISEASE: the more active NA-1 allele has been associated with  
 CC severe renal disease in certain systemic vasculitides.  
 CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES:  
 CC FCG3A AND FCG3B (SHOWN HERE) WHICH ARE EXPRESSED IN A TISSUE-  
 CC SPECIFIC MANNER. THE PHE-203 IN FCG3A DETERMINES THE  
 CC TRANSMEMBRANE DOMAINS WHEREAS THE SER-203 IN FCG3B DETERMINES THE  
 CC GPI-ANCHORING.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD16B entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd16b.htm".  
 CC -----  
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 CC -----  
 CC EMBL; X16863; CAA34753.1; -;  
 CC EMBL; X07934; CAA30788.1; -;  
 CC EMBL; J04162; AAA35881.1; -;  
 CC EMBL; Z46223; CAA86296.1; -;  
 CC PIR; J00284; J00284;  
 CC PDB; 1E4J; 04-AUG-00.  
 CC PDB; 1E4K; 06-JUN-01.  
 CC PDB; 1E4L; 22-NOV-00.  
 CC PDB; 1I1S; 16-MAY-01.  
 CC PDB; 1I1X; 16-MAY-01.  
 CC Genev; HGNC:3620; FCG3B.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC InterPro; IPR007110; Ig-like.  
 CC InterPro; IPR003599; Ig.  
 CC Pfam; PF00047; Ig; 2.  
 CC SMART; SM00409; Ig; 2.  
 CC PROSITE; PSS0835; Ig-Like; 1.  
 CC IGG-binding protein; Receptor; GPI-anchor; Glycoprotein; Signal;  
 CC Immunoglobulin domain; Repeat; Multigene family; Polymorphism;  
 CC 3D-structure; Lipoprotein.  
 CC FT SIGNAL 1 16  
 CC FT CHAIN 17 200  
 CC  
 CC FT PROPEP 201 233  
 CC FT LIPID 200 200  
 CC FT DOMAIN 40 96  
 CC FT DOMAIN 121 179  
 CC FT DISULFID 47 89  
 CC FT DISULFID 128 172  
 CC FT CARBOHYD 56 56  
 CC FT CARBOHYD 63 63  
 CC FT CARBOHYD 82 82  
 CC FT CARBOHYD 92 92  
 CC FT CARBOHYD 180 180  
 CC FT CARBOHYD 187 187  
 CC FT VARIANT 36 36  
 CC  
 CC FT VARIANT 65 65  
 CC FT VARIANT 78 78  
 CC FT VARIANT 82 82  
 CC FT VARIANT 106 106  
 CC  
 CC FT SEQUENCE 233 AA; 26216 MW; 7AB5159432761726 CRC64;  
 CC  
 CC Query Match 33.9%; Score 363.5; DB 1; Length 233;  
 CC Best Local Similarity 42.8%; Pred. No. 1e-24;  
 CC Matches 80; Conservative 26; Mismatches 78; Indels 3; Gaps 2;  
 CC  
 CC 10 LLCVALLFPADGVLAQPKK--VSLNPPNWRKFGENTVLTCTGNFFVSTKGFHN 67

Db 5 LPTALLLVASAG-MRTEDLPKAVFLEFQWYSLKSDSVTLKCOQAYSPEDNSTGFHN 63  
 Qy 68 GSLSEETNSLNIVNAKFEDSGEYKQHQQVNESEPVYLEVFSMDWLLLOASAEVWEGQP 127  
 Db 64 ESLISSQASSYFIDAATVNDSGEYRCQTNLSLSDPVLQLEHIGWLLLOAPRWVFEEDP 123  
 Qy 128 LFLRCHGRWMDVKKIYYKDGKALXYWENHISITNATVEDSGTYCTGKWLQDYES 187  
 Db 124 IHLRCHSKNTALHKVYTLQNGKDRKYFHNSDFHPKATLKDSGYSFCEGLVGSKNVSS 183  
 Qy 188 EPLNITV 194  
 Db 184 ETVNITI 190  
 RESULT 14  
 FCG3 RAT  
 ID\_FCG3 RAT STANDARD; PRT; 267 AA.  
 AC P27645; Q04798; Q63204;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, last sequence update)  
 DT 10-OCT-2003 (Rel. 42, last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region receptor III precursor  
 DE (IGG Fc receptor III) (FC-gamma RIII) (FCRIII).  
 GN FCGR3.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=91250730; PubMed=1710249;  
 RA Farber D.L., Sears D.W.;  
 RT "Rat CD16 is defined by a family of class III Fc gamma receptors  
 RT requiring co-expression of heteroprotein subunits.";  
 RL J. Immunol. 146:4352-4361(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=Natural killer cells;  
 RX MEDLINE=90239026; PubMed=1692135;  
 RA Zeger D.L., Hogarth P.M., Sears D.W.;  
 RT "Characterization and expression of an Fc gamma receptor cDNA cloned  
 RT from rat natural killer cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM H).  
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
 RX MEDLINE=93246650; PubMed=8482840;  
 RA Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P.,  
 RA Sears D.W.;  
 RT "Rat class III Fc gamma receptor isoforms differ in igg subclass-  
 RT binding specificity and fail to associate productively with rat CD3  
 RT zeta.";  
 RL J. Immunol. 150:4364-4375(1993).  
 CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins  
 CC gamma. Low affinity receptor.  
 CC -!- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS.  
 CC THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE  
 CC EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=8;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=C;  
 CC IsoId=P27645-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=P27645-3; Sequence=Not described;  
 CC Name=B;  
 CC IsoId=P27645-4; Sequence=Not described;  
 CC Name=D;  
 CC IsoId=P27645-5; Sequence=Not described;  
 CC











Result No.	Score	Query Match	Length	ID	Description
1	618	57.6	260	QSMJ20	Q8m120 ovis aries
2	617	57.5	255	QSM130	Q8m130 equus caball
3	383.5	35.7	357	Q8SPW5	Q8SPW5 macaca fasc
4	378.5	35.3	349	Q8MZ10	Q8m210 bos taurus
5	376	35.0	374	Q92663	Q92663 homo sapien
6	375.5	35.0	280	Q4Q2637	Q92637 homo sapien
7	375.5	35.0	4	Q92495	Q92495 homo sapien
8	374.5	34.9	294	Q8SPW3	Q8SPW3 macaca fasc
9	373.5	34.8	330	Q8R142	Q8r142 mus musculus
10	369.5	34.4	254	Q8SPW2	Q8SPW2 macaca fasc
11	367	34.2	249	Q8R477	Q8r477 mus musculus
12	366.5	34.2	372	Q7YQJ5	Q7Yqj5 canis famul
13	365	34.0	249	Q8R2R4	Q8r2r4 mus musculus
14	363	33.8	249	Q9N216	Q9n216 felis silve
15	363	33.8	261	Q9ES92	Q9es92 mus musculus
16	359.5	33.5	233	Q9UPY7	Q9upy7 homo sapien

Db 6 MGAPALLMIALLLFSPDGSAAWKSIVSLNPPWREIFRGETVTLTTCGVRSSSESSVW 65  
 QY 65 FINGSLSEBTNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAEVWME 124  
 Db 66 IINGTILKETNRWDIVKARVODSGYKQRIKGFAPISBPVYLNVISDWLLILQASAEVWME 125  
 QY 125 GQPLFLRCHGWRNDVYKVIYVYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMOLD 184  
 Db 126 GESLFLRCHSWKLNFAKVIYVYKDNRAKYWYENHNISITNATVEDSGTYCTGKVMOLD 185  
 QY 185 YESEPLNITVIK 196  
 Db 186 YTSNKLKIIVK 197

## RESULT 2

QBM130  
 ID Q8M130 PRELIMINARY; PRT; 255 AA.  
 AC Q8M130;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE High affinity immunoglobulin E receptor alpha subunit.  
 OS Equus caballus (Horse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;  
 RX MEDLINE=20424522; PubMed=10970105;  
 RA McAllee S.M., Halliwell R.E.W., Miller H.R.P.;  
 RT "Cloning and Sequencing of the horse and sheep high-affinity Ige  
 receptor alpha chain cDNA";  
 RL Immunogenetics 51:878-881(2000).  
 DR EMBL; Y18204; CAB40387.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; IG\_1-like.  
 DR InterPro; IPR007110; IG\_1-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00408; IGC2; 2.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR Immunoglobulin domain; Receptor.  
 KW Immunoglobulin domain; Receptor.  
 SQ SEQUENCE 255 AA; 29366 MW; A60659700684FBD8 CRC64;

Query Match 57.5%; Score 617; DB 6; Length 255;  
 Best Local Similarity 60.2%; Pred. No. 1.4e-48;  
 Matches 121; Conservative 24; Mismatches 52; Indels 4; Gaps 1;  
 QY 1 MAPAMESPTLLCVALLFFAPDGLVAVPQKPKVSLNPPWNRIFKGENVTITCNKNPFVVS 60  
 Db 1 MPAPMGSPALLWTITFLFLSDGLGVPFAIRKSTVSLNPPWNRIFKGENVTITCNKNKPLKGN 60  
 QY 61 STKWFHNGSLSEBTNSLNIIVNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAE 120  
 Db 61 STEWYNTTLEVTSSLTNITNASHSSGEYRCRNDNLSEAVHLEVPDMLILQASAE 120  
 QY 121 VVMEGQPLRCHGWRNDVYKVIYVYKDGKALKYWYENHNISITNATVEDSGTYCTG-- 178  
 Db 121 EVIEGKALVLRCKGWKDWDFKVIYVYKDGKFLPYWYENKNISIESATTENSCTYCEGAF 180  
 QY 179 --KVMOLDYESEPLNITVKA 197  
 Db 181 NFKRTSERTSDVLTNITVKA 201

## RESULT 3

Q8SPW5  
 ID Q8SPW5 PRELIMINARY; PRT; 357 AA.  
 AC Q8SPW5;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 GN Fc gamma receptor I.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,  
 RA Presta L.G.;  
 RT "Binding of human IgG to cynomolgus FcR.";  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF485812; AAL92095.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00409; Ig; 3.  
 DR PROSITE; PS00835; IG LIKE; 3.  
 KW Receptor.  
 SQ SEQUENCE 357 AA; 40715 MW; F5C51A06A3BCB08F CRC64;  
 Query Match 35.7%; Score 383.5; DB 6; Length 357;  
 Best Local Similarity 40.7%; Pred. No. 5.8e-27;  
 Matches 74; Conservative 38; Mismatches 67; Indels 3; Gaps 3;  
 QY 14 ALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTITCNKNPFVVSSTKWFHNGSLSE 72  
 Db 6 ALLLVPPDGGVDT-TKAVITLQPPWVSFQEEVTTLQCEVPLPGSSSTQWFLNGATQ 64  
 QY 73 ETNSSLNIIVNAKFDSEYKCOHQVNESEPVYLEVPSDWLLILQASAEVMEGQPLFIRC 132  
 Db 65 TSTPSYRITSASVSDSGEYRCQGPSGRSDPIQIEHRDMLLLQVSRVTEGEPLALRC 124  
 QY 133 HGRNWDVYKVIYVYKDGKALKYWYENHNISITNATVEDSGTYCTGKVMOLDYESEPLNI 192  
 Db 125 HAWKDKLVYVYVYQNGKAPKFFYRNSQLTILTKNISHNGAYHCSG-MGXHYTSAGVSV 183  
 QY 193 TV 194  
 Db 184 TV 185  
 RESULT 4  
 Q8MZTO PRELIMINARY; PRT; 349 AA.  
 ID Q8MZTO  
 AC Q8MZTO;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Fc gamma receptor I.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20349800; PubMed=10899306;  
 RA Yan Y., Li X., Wang A., Zhang G.;  
 RT "Molecular cloning and identification of full-length cDNA encoding  
 high affinity Fc receptor for bovine IgG (Fc gamma RI).";  
 RL Vet. Immunol. Immunopathol. 75:151-159(2000).  
 DR EMBL; AF162866; AAF80477.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00408; IGC2; 1.

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DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 349 AA; 39608 MW; D0B77B2EF9408C02 CRC64;

Query Match 35.3%; Score 378.5; DB 6; Length 349;
Best Local Similarity 40.2%; Pred. No. 1.6e-26;
Matches 74; Conservative 38; Mismatches 71; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGNVTLCNGNNFFVSVSTKWFNGSL 70
Db 3 LIALILGAPVAEQVDPTKAVITLKPPWVSFQENVTLLCEGPHRPGDTATQWFLNGTA 62
QY 71 SEETNSLNIIVNAKPEDSGEYKQHQVNESEPVYLFVFSDWLLQLQASAVVMEGQPLFL 130
Db 63 IKTLPARYSINATDDSGEYKQGLNLSQVLEHSDWLLQLQVTSRVFTGEPPLAL 122
QY 131 RCHGRNWDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKQWQLDYSEPL 190
Db 123 RCHAWKQKLVNVLVYRNGKAFKFFHWNSTILKTNISHNGTYHCSG-RRRYTSAGV 181

QY 191 NITV 194
Db 182 SVTV 185

RESULT 5
Q92663 PRELIMINARY; PRT; 374 AA.
AC Q92663;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor I.
GN Al.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Porges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03418; AAA36049.1; -.
DR PIR; A39878; A39878.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; IG_3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 374 AA; 42632 MW; D33D59398CEBA699 CRC64;

Query Match 35.0%; Score 376; DB 4; Length 374;
Best Local Similarity 39.7%; Pred. No. 3e-26;
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGNVTLCNGNNFFVSVSTKWFNGSL 70
Db 4 LTTLLWVPDGVQVDT-TRAVITLQPPWVSFQETVTLHCEVHLHFGSSSTQWFLNGTA 62
QY 71 SEETNSLNIIVNAKPEDSGEYKQHQVNESEPVYLFVFSDWLLQLQASAVVMEGQPLFL 130
Db 63 TQTSYRITSASVNDSEYRCQGLSGRSDPIQLIHRGWLQLQVSSRVFTEGEPPLAL 122
QY 131 RCHGRNWDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKQWQLDYSEPL 190
Db 123 RCHAWKQKLVNVLVYRNGKAFKFFHWNSTILKTNISHNGTYHCSG-MGKHRYTSAGI 181
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QY 191 NITV 194
Db 182 SVTV 185

RESULT 6
Q92637 PRELIMINARY; PRT; 280 AA.
AC Q92637;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor I.
GN B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93055454; PubMed=1430234;
RA Porges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA Kimberly R.P.;
RT "Novel Fc gamma receptor I family gene products in human mononuclear
RT cells.";
RL J. Clin. Invest. 90:2102-2109(1992).
DR EMBL; L03419; AAA35825.1; -.
DR PIR; A55577; A55577.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Receptor.
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AB3D345C6 CRC64;

Query Match 35.0%; Score 375.5; DB 4; Length 280;
Best Local Similarity 41.7%; Pred. No. 2.3e-26;
Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;

QY 11 LCVALFFAPDGLVAVPQPKVSLNPPWNRIFKGNVTLCNGNNFFVSVSTKWFNGSL 70
Db 4 LTTLLWVPDGVQVDT-TRAVITLQPPWVSFQETVTLHCEVHLHFGSSSTQWFLNGTA 62
QY 71 SEETNSLNIIVNAKPEDSGEYKQHQVNESEPVYLFVFSDWLLQLQASAVVMEGQPLFL 130
Db 63 TQTSYRITSASVNDSEYRCQGLSGRSDPIQLIHRGWLQLQVSSRVFTEGEPPLAL 122
QY 131 RCHGRNWDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTG 178
Db 123 RCHAWKQKLVNVLVYRNGKAFKFFHWNSTILKTNISHNGTYHCSG 170

RESULT 7
Q92495 PRELIMINARY; PRT; 375 AA.
AC Q92495;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE FC gamma receptor type I (FC gamma RIB=FC gamma receptor).
GN CD64 OR FC<GAMMA>RIB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Ravesh D.,  
 RA Ezekowitz A.B.;  
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 1-224 FROM N.A.  
 RX MEDLINE=93018827; PubMed=1402657;  
 RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Ravesh D.P.,  
 RA Ezekowitz R.A.;  
 RT "Definition of interferon gamma-response elements in a novel human Fc  
 gamma receptor gene (Fc gamma R1b) and characterization of the gene  
 structure.";  
 RT J. Exp. Med. 176:1115-1123 (1992).  
 RL EMBL; M91555; AAA58414.1; JOINED.  
 DR EMBL; M91550; AAA58414.1; JOINED.  
 DR EMBL; M91553; AAA58414.1; JOINED.  
 DR EMBL; M91552; AAA58414.1; JOINED.  
 DR EMBL; M91553; AAA58414.1; JOINED.  
 DR EMBL; M91554; AAA58414.1; JOINED.  
 DR EMBL; M91555; AAA58414.1; JOINED.  
 DR EMBL; S45709; AAD13842.1; JOINED.  
 DR EMBL; S45707; AAD13842.1; JOINED.  
 DR EMBL; S45708; AAD13842.1; JOINED.  
 DR EMBL; S45704; AAD13842.1; JOINED.  
 DR EMBL; S45705; AAD13842.1; JOINED.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 3.  
 KW Immunoglobulin domain.  
 SQ SEQUENCE 375 AA; 42881 MW; A84D464C70DD0F91 CRC64;  
 Query Match 35.0%; Score 375.5; DB 4; Length 375;  
 Best Local Similarity 41.7%; Pred. No. 3.3e-26;  
 Matches 70; Conservative 34; Mismatches 63; Indels 1; Gaps 1;  
 QY 11 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSVSTKWFHNGSL 70  
 DB 4 LITLLVWPVGVDVTRKAVITLQPPWVSVFQSEVTLHCEVLELPGSSSTQWFLNGTA 62  
 QY 71 SEETNSLNVNAKPEDSGEYKCOHQVNESEPPVLEVPFSDWLLLOASAEVVMGQPLFL 130  
 DB 63 TOTSTPSYRITSASVNDSEYRCQGLSGRSDPEIQLEIHRGWLLOVSSRVFMEGEPTAL 122  
 QY 131 RCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG 178  
 DB 123 RCHAWKDKLVNVLVYRNGAKKFFPHNSNLTLKTNISNGTHCSG 170  
 RESULT 8  
 Q8SPW3 PRELIMINARY; PRT; 294 AA.  
 AC Q8SPW3  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Fc gamma receptor IIB.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Nameruk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,  
 RA Presta L.G.;  
 RT "Binding of human IgG to cynomolgus FcR";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF485814; AAL92097.1;  
 DR GO; GO:0004872; Fc receptor activity; IEA.  
 DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 KW Receptor.  
 SQ SEQUENCE 294 AA; 32151 MW; A8D476A448E3D01E CRC64;  
 Query Match 34.9%; Score 374.5; DB 6; Length 294;  
 Best Local Similarity 40.3%; Pred. No. 3e-26;  
 Matches 75; Conservative 32; Mismatches 78; Indels 1; Gaps 1;  
 QY 10 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSVSTKWFHNG 68  
 DB 29 LITLLVWPVGVDVTRKAVITLQPPWVSVFQSEVTLHCEVLELPGSSSTQWFLNGTA 88  
 QY 69 SEETNSLNVNAKPEDSGEYKCOHQVNESEPPVLEVPFSDWLLLOASAEVVMGQPL 128  
 DB 89 NLIPHTQPSYRITSASVNDSEYRCQGLSGRSDPEIQLEIHRGWLLOVSSRVFMEGEPTAL 148  
 QY 129 FLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG 188  
 DB 149 LLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG 208  
 QY 189 PLNITV 194  
 DB 209 PVTITV 214  
 RESULT 9  
 Q8R142 PRELIMINARY; PRT; 330 AA.  
 AC Q8R142  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025535; AAH25535.1;  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 KW Hypothetical protein; Immunoglobulin domain.  
 FT NON TER 1  
 SQ SEQUENCE 330 AA; 37116 MW; 891F8724F870D88E CRC64;  
 Query Match 34.8%; Score 373.5; DB 11; Length 330;  
 Best Local Similarity 42.5%; Pred. No. 4.3e-26;  
 Matches 79; Conservative 35; Mismatches 69; Indels 3; Gaps 3;  
 QY 10 LCVALFFAPDGVLAVPQPKVSLNPPWNRIFKGNVLTTCNGNNFFVSVSTKWFHNGS 69  
 DB 6 LITLLVWPVGVDVTRKAVITLQPPWVSVFQSEVTLHCEVLELPGSSSTQWFLNGTA 65  
 QY 70 SEETNSLNVNAKPEDSGEYKCOHQVNESEPPVLEVPFSDWLLLOASAEVVMGQPL 128  
 DB 66 VQISTPSYRITSASVNDSEYRCQGLSGRSDPEIQLEIHRGWLLOVSSRVFMEGEPTAL 125  
 QY 129 FLRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG 188  
 DB 126 ALRCHGWRNDVYKVIYKDGKALKYWYENHNISITNATVEDSGTYCTG 183  
 QY 189 PLNITV 194  
 DB 184 GVSTIV 189